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(54) Title: SECRETORY MOLECULES

(57) Abstract: The present invention provides purified secretory polynucleotides (sptm). Also encompassed are the polypeptides (SPTM) encoded by sptm. The invention also provides for the use of sptm, or complements, oligonucleotides, or fragments thereof in diagnostic assays. The invention further provides for vectors and host cells containing sptm for the expression of SPTM. The invention additionally provides for the use of isolated and purified SPTM to induce antibodies and to screen libraries of compounds and the use of anti-SPTM antibodies in diagnostic assays. Also provided are microarrays containing sptm and methods of use.

SECRETORY MOLECULES

TECHNICAL FIELD

The present invention relates to secretory molecules and to the use of these sequences in the diagnosis, study, prevention, and treatment of diseases associated with cell signaling.

BACKGROUND OF THE INVENTION

Protein transport and secretion are essential for cellular function. Protein transport is mediated by a signal peptide located at the amino terminus of the protein to be transported or secreted. The signal peptide is comprised of about ten to twenty hydrophobic amino acids which target the nascent protein from the ribosome to a particular membrane bound compartment such as the endoplasmic reticulum (ER). Proteins targeted to the ER may either proceed through the secretory pathway or remain in any of the secretory organelles such as the ER, Golgi apparatus, or lysosomes. Proteins that transit through the secretory pathway are either secreted into the extracellular space or retained in the plasma membrane. Proteins that are retained in the plasma membrane contain one or more transmembrane domains, each comprised of about 20 hydrophobic amino acid residues. Proteins that are secreted from the cell are generally synthesized as inactive precursors that are activated by post-translational processing events during transit through the secretory pathway. Such events include glycosylation, proteolysis, and removal of the signal peptide by a signal peptidase. Other events that may occur during protein transport include chaperone-dependent unfolding and folding of the nascent protein and interaction of the protein with a receptor or pore complex. Examples of secretory proteins with amino terminal signal peptides are discussed below and include proteins with important roles in cell-to-cell signaling. Such proteins include transmembrane receptors and cell surface markers, extracellular matrix molecules, cytokines, hormones, growth and differentiation factors, neuropeptides, vasomediators, ion channels, transporters/pumps, and proteases. (Reviewed in Alberts, B. et al. (1994) Molecular Biology of The Cell, Garland Publishing, New York, NY, pp. 557-560, 582-592.)

G-protein coupled receptors (GPCRs) comprise a superfamily of integral membrane proteins which transduce extracellular signals. Not all GPCRs contain N-terminal signal peptides. GPCRs include receptors for biogenic amines such as dopamine, epinephrine, histamine, glutamate (metabotropic-type), acetylcholine (muscarinic-type), and serotonin; for lipid mediators of inflammation such as prostaglandins, platelet activating factor, and leukotrienes; for peptide hormones such as calcitonin, C5a anaphylatoxin, follicle stimulating hormone, gonadotropin releasing hormone, neurokinin, oxytocin, and thrombin; and for sensory signal mediators such as retinal photopigments and olfactory stimulatory molecules. The structure of these highly conserved receptors consists of seven hydrophobic transmembrane regions, cysteine disulfide bridges between

the second and third extracellular loops, an extracellular N-terminus, and a cytoplasmic C-terminus. The N-terminus interacts with ligands, the disulfide bridges interact with agonists and antagonists, and the large third intracellular loop interacts with G proteins to activate second messengers such as cyclic AMP, phospholipase C, inositol triphosphate, or ion channels. (Reviewed in Watson, S. and Arkinstall, S. (1994) The G-protein Linked Receptor Facts Book, Academic Press, San Diego, CA, pp. 2-6; and Bolander, F.F. (1994) Molecular Endocrinology, Academic Press, San Diego, CA, pp. 162-176.)

Other types of receptors include cell surface antigens identified on leukocytic cells of the immune system. These antigens have been identified using systematic, monoclonal antibody (mAb)-based "shot gun" techniques. These techniques have resulted in the production of hundreds of mAbs directed against unknown cell surface leukocytic antigens. These antigens have been grouped into "clusters of differentiation" based on common immunocytochemical localization patterns in various differentiated and undifferentiated leukocytic cell types. Antigens in a given cluster are presumed to identify a single cell surface protein and are assigned a "cluster of differentiation" or "CD" designation. Some of the genes encoding proteins identified by CD antigens have been cloned and verified by standard molecular biology techniques. CD antigens have been characterized as both transmembrane proteins and cell surface proteins anchored to the plasma membrane via covalent attachment to fatty acid-containing glycolipids such as glycosylphosphatidylinositol (GPI). (Reviewed in Barclay, A. N. et al. (1995) The Leucocyte Antigen Facts Book, Academic Press, San Diego, CA, pp. 17-20.)

Matrix proteins (MPs) are transmembrane and extracellular proteins which function in formation, growth, remodeling, and maintenance of tissues and as important mediators and regulators of the inflammatory response. The expression and balance of MPs may be perturbed by biochemical changes that result from congenital, epigenetic, or infectious diseases. In addition, MPs affect leukocyte migration, proliferation, differentiation, and activation in the immune response. MPs are frequently characterized by the presence of one or more domains which may include collagen-like domains, EGF-like domains, immunoglobulin-like domains, and fibronectin-like domains. In addition, MPs may be heavily glycosylated and may contain an Arginine-Glycine-Aspartate (RGD) tripeptide motif which may play a role in adhesive interactions. MPs include extracellular proteins such as fibronectin, collagen, galectin, vitronectin and its proteolytic derivative somatomedin B; and cell adhesion receptors such as cell adhesion molecules (CAMs), cadherins, and integrins. (Reviewed in Ayad, S. et al. (1994) The Extracellular Matrix Facts Book, Academic Press, San Diego, CA, pp. 2-16; Ruoslahti, E. (1997) Kidney Int. 51:1413-1417; Sjaastad, M.D. and Nelson, W.J. (1997) BioEssays 19:47-55.)

Cytokines are secreted by hematopoietic cells in response to injury or infection. Interleukins, neurotrophins, growth factors, interferons, and chemokines all define cytokine families that work in

conjunction with cellular receptors to regulate cell proliferation and differentiation. In addition, cytokines effect activities such as leukocyte migration and function, hematopoietic cell proliferation, temperature regulation, acute response to infection, tissue remodeling, and apoptosis.

Chemokines, in particular, are small chemoattractant cytokines involved in inflammation, leukocyte proliferation and migration, angiogenesis and angiostasis, regulation of hematopoiesis, HIV infectivity, and stimulation of cytokine secretion. Chemokines generally contain 70-100 amino acids and are subdivided into four subfamilies based on the presence of conserved cysteine-based motifs. (Callard, R. and Gearing, A. (1994) The Cytokine Facts Book, Academic Press, New York, NY, pp. 181-190, 210-213, 223-227.)

Growth and differentiation factors are secreted proteins which function in intercellular communication. Some factors require oligomerization or association with MPs for activity. Complex interactions among these factors and their receptors trigger intracellular signal transduction pathways that stimulate or inhibit cell division, cell differentiation, cell signaling, and cell motility. Most growth and differentiation factors act on cells in their local environment (paracrine signaling). There are three broad classes of growth and differentiation factors. The first class includes the large polypeptide growth factors such as epidermal growth factor, fibroblast growth factor, transforming growth factor, insulin-like growth factor, and platelet-derived growth factor. The second class includes the hematopoietic growth factors such as the colony stimulating factors (CSFs). Hematopoietic growth factors stimulate the proliferation and differentiation of blood cells such as B-lymphocytes, T-lymphocytes, erythrocytes, platelets, eosinophils, basophils, neutrophils, macrophages, and their stem cell precursors. The third class includes small peptide factors such as bombesin, vasopressin, oxytocin, endothelin, transferrin, angiotensin II, vasoactive intestinal peptide, and bradykinin which function as hormones to regulate cellular functions other than proliferation.

Growth and differentiation factors play critical roles in neoplastic transformation of cells in vitro and in tumor progression in vivo. Inappropriate expression of growth factors by tumor cells may contribute to vascularization and metastasis of tumors. During hematopoiesis, growth factor misregulation can result in anemias, leukemias, and lymphomas. Certain growth factors such as interferon are cytotoxic to tumor cells both in vivo and in vitro. Moreover, some growth factors and growth factor receptors are related both structurally and functionally to oncoproteins. In addition, growth factors affect transcriptional regulation of both proto-oncogenes and oncosuppressor genes. (Reviewed in Pimentel, E. (1994) Handbook of Growth Factors, CRC Press, Ann Arbor, MI, pp. 1-9.)

Proteolytic enzymes or proteases either activate or deactivate proteins by hydrolyzing peptide bonds. Proteases are found in the cytosol, in membrane-bound compartments, and in the extracellular space. The major families are the zinc, serine, cysteine, thiol, and carboxyl proteases.

Ion channels, ion pumps, and transport proteins mediate the transport of molecules across cellular membranes. Transport can occur by a passive, concentration-dependent mechanism or can be

linked to an energy source such as ATP hydrolysis. Symporters and antiporters transport ions and small molecules such as amino acids, glucose, and drugs. Symporters transport molecules and ions unidirectionally, and antiporters transport molecules and ions bidirectionally. Transporter superfamilies include facilitative transporters and active ATP-binding cassette transporters which are involved in multiple-drug resistance and the targeting of antigenic peptides to MHC Class I molecules. These transporters bind to a specific ion or other molecule and undergo a conformational change in order to transfer the ion or molecule across the membrane. (Reviewed in Alberts, B. et al. (1994) Molecular Biology of The Cell, Garland Publishing, New York, NY, pp. 523-546.)

Ion channels are formed by transmembrane proteins which create a lined passageway across the membrane through which water and ions, such as Na^+, K^+, Ca^{2+}, and Cl^-, enter and exit the cell. For example, chloride channels are involved in the regulation of the membrane electric potential as well as absorption and secretion of ions across the membrane. Chloride channels also regulate the internal pH of membrane-bound organelles.

Ion pumps are ATPases which actively maintain membrane gradients. Ion pumps are classified as P, V, or F according to their structure and function. All have one or more binding sites for ATP in their cytosolic domains. The P-class ion pumps include Ca^{2+} ATPase and Na^+/K^+ ATPase and function in transporting H^+, Na^+, K^+, and Ca^{2+} ions. P-class pumps consist of two α and two β transmembrane subunits. The V- and F-class ion pumps have similar structures but transport only H^+. F class H^+ pumps mediate transport across the membranes of mitochondria and chloroplasts, while V-class H^+ pumps regulate acidity inside lysosomes, endosomes, and plant vacuoles.

A family of structurally related intrinsic membrane proteins known as facilitative glucose transporters catalyze the movement of glucose and other selected sugars across the plasma membrane. The proteins in this family contain a highly conserved, large transmembrane domain comprised of 12 α-helices, and several weakly conserved, cytoplasmic and exoplasmic domains. (Pessin, J. E., and Bell, G.I. (1992) Annu. Rev. Physiol. 54:911-930.)

Amino acid transport is mediated by Na^+ dependent amino acid transporters. These transporters are involved in gastrointestinal and renal uptake of dietary and cellular amino acids and in neuronal reuptake of neurotransmitters. Transport of cationic amino acids is mediated by the system y+ family and the cationic amino acid transporter (CAT) family. Members of the CAT family share a high degree of sequence homology, and each contains 12-14 putative transmembrane domains. (Ito, K. and Groudine, M. (1997) J. Biol. Chem. 272:26780-26786.)

Hormones are secreted molecules that travel through the circulation and bind to specific receptors on the surface of, or within, target cells. Although they have diverse biochemical compositions and mechanisms of action, hormones can be grouped into two categories. One category includes small lipophilic hormones that diffuse through the plasma membrane of target cells, bind to cytosolic or nuclear receptors, and form a complex that alters gene expression. Examples of these

molecules include retinoic acid, thyroxine, and the cholesterol-derived steroid hormones such as progesterone, estrogen, testosterone, cortisol, and aldosterone. The second category includes hydrophilic hormones that function by binding to cell surface receptors that transduce signals across the plasma membrane. Examples of such hormones include amino acid derivatives such as catecholamines and peptide hormones such as glucagon, insulin, gastrin, secretin, cholecystokinin, adrenocorticotropic hormone, follicle stimulating hormone, luteinizing hormone, thyroid stimulating hormone, and vasopressin. (See, for example, Lodish et al. (1995) Molecular Cell Biology, Scientific American Books Inc., New York, NY, pp. 856-864.)

Neuropeptides and vasomediators (NP/VM) comprise a large family of endogenous signaling molecules. Included in this family are neuropeptides and neuropeptide hormones such as bombesin, neuropeptide Y, neurotensin, neuromedin N, melanocortins, opioids, galanin, somatostatin, tachykinins, urotensin II and related peptides involved in smooth muscle stimulation, vasopressin, vasoactive intestinal peptide, and circulatory system-borne signaling molecules such as angiotensin, complement, calcitonin, endothelins, formyl-methionyl peptides, glucagon, cholecystokinin and gastrin. NP/VMs can transduce signals directly, modulate the activity or release of other neurotransmitters and hormones, and act as catalytic enzymes in cascades. The effects of NP/VMs range from extremely brief to long-lasting. (Reviewed in Martin, C. R. et al. (1985) Endocrine Physiology, Oxford University Press, New York, NY, pp. 57-62.)

The discovery of new secretory molecules satisfies a need in the art by providing new compositions which are useful in the diagnosis, study, prevention, and treatment of diseases associated with cell signaling.

SUMMARY OF THE INVENTION

The present invention relates to nucleic acid sequences comprising human polynucleotides encoding secretory polypeptides that contain signal peptides and/or transmembrane domains. These human polynucleotides (sptm) as presented in the Sequence Listing uniquely identify genes encoding structural, functional, and regulatory polypeptides (SPTM) involved in cell signaling.

The invention provides an isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of a) a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-26; b) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-26; c) a polynucleotide sequence complementary to a); d) a polynucleotide sequence complementary to b); and e) an RNA equivalent of a) through d). In one alternative, the polynucleotide comprises a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-26. In another alternative, the polynucleotide comprises at least 60 contiguous nucleotides of a polynucleotide sequence selected from the group consisting of a) a polynucleotide sequence selected from the group

consisting of SEQ ID NO:1-26; b) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-26; c) a polynucleotide sequence complementary to a); d) a polynucleotide sequence complementary to b); and e) an RNA equivalent of a) through d). The invention further provides a composition for the detection of expression of secretory polynucleotides comprising at least one isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of a) a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-26; b) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-26; c) a polynucleotide sequence complementary to a); d) a polynucleotide sequence complementary to b); and e) an RNA equivalent of a) through d); and a detectable label.

The invention also provides a method for detecting a target polynucleotide in a sample, said target polynucleotide comprising a polynucleotide sequence selected from the group consisting of a) a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-26; b) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-26; c) a polynucleotide sequence complementary to a); d) a polynucleotide sequence complementary to b); and e) an RNA equivalent of a) through d). The method comprises a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide, and b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof. In one alternative, the probe comprises at least 30 contiguous nucleotides. In another alternative, the probe comprises at least 60 contiguous nucleotides.

The invention further provides a recombinant polynucleotide comprising a promoter sequence operably linked to an isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of a) a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-26; b) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-26; c) a polynucleotide sequence complementary to a); d) a polynucleotide sequence complementary to b); and e) an RNA equivalent of a) through d). In one alternative, the invention provides a cell transformed with the recombinant polynucleotide. In another alternative, the invention provides a transgenic organism comprising the recombinant polynucleotide. In a further alternative, the invention provides a method for producing a secretory polypeptide, the method comprising a) culturing a cell under conditions suitable for expression of the secretory polypeptide, wherein said cell is transformed with the recombinant polynucleotide, and b) recovering the secretory polypeptide so expressed.

The invention also provides a purified secretory polypeptide (SPTM) encoded by at least one polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-26. Additionally, the invention provides an isolated antibody which specifically binds to the secretory polypeptide. The invention further provides a method of identifying a test compound which specifically binds to the secretory polypeptide, the method comprising the steps of a) providing a test compound; b) combining the secretory polypeptide with the test compound for a sufficient time and under suitable conditions for binding; and c) detecting binding of the secretory polypeptide to the test compound, thereby identifying the test compound which specifically binds the secretory polypeptide.

The invention further provides a microarray wherein at least one element of the microarray is an isolated polynucleotide comprising at least 60 contiguous nucleotides of a polynucleotide comprising a polynucleotide sequence selected from the group consisting of a) a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-26; b) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-26; c) a polynucleotide sequence complementary to a); d) a polynucleotide sequence complementary to b); and e) an RNA equivalent of a) through d). The invention also provides a method for generating a transcript image of a sample which contains polynucleotides. The method comprises a) labeling the polynucleotides of the sample, b) contacting the elements of the microarray with the labeled polynucleotides of the sample under conditions suitable for the formation of a hybridization complex, and c) quantifying the expression of the polynucleotides in the sample.

Additionally, the invention provides a method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a polynucleotide sequence selected from the group consisting of a) a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-26; b) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-26; c) a polynucleotide sequence complementary to a); d) a polynucleotide sequence complementary to b); and e) an RNA equivalent of a) through d). The method comprises a) exposing a sample comprising the target polynucleotide to a compound, and b) detecting altered expression of the target polynucleotide.

The invention further provides a method for detecting a target polynucleotide in a sample for toxicity testing of a compound, said target polynucleotide comprising a polynucleotide sequence selected from the group consisting of a) a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-26; b) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-26; c) a polynucleotide sequence complementary to a); d) a polynucleotide sequence complementary to b); and e) an RNA equivalent of a) through d). The method comprises a) hybridizing the sample with a

probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide, b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof, and c) comparing the presence, absence or amount of said target polynucleotide in a first biological sample and a second biological sample, wherein said first biological sample has been contacted with said compound, and said second sample is a control, whereby a change in presence, absence or amount of said target polynucleotide in said first sample, as compared with said second sample, is indicative of toxic response to said compound.

DESCRIPTION OF THE TABLES

Table 1 shows the sequence identification numbers (SEQ ID NO:s) and template identification numbers (template IDs) corresponding to the polynucleotides of the present invention, along with their GenBank hits (GI Numbers), probability scores, and functional annotations corresponding to the GenBank hits.

Table 2 shows the sequence identification numbers (SEQ ID NO:s) and template identification numbers (template IDs) corresponding to the polynucleotides of the present invention, along with polynucleotide segments of each template sequence as defined by the indicated "start" and "stop" nucleotide positions. The reading frames of the polynucleotide segments are shown, and the polypeptides encoded by the polynucleotide segments constitute either signal peptide (SP) or transmembrane (TM) domains, as indicated.

Table 3 shows the sequence identification numbers (SEQ ID NO:s) and template identification numbers (template IDs) corresponding to the polynucleotides of the present invention, along with component sequence identification numbers (component IDs) corresponding to each template. The component sequences, which were used to assemble the template sequences, are defined by the indicated "start" and "stop" nucleotide positions along each template.

Table 4 summarizes the bioinformatics tools which are useful for analysis of the polynucleotides of the present invention. The first column of Table 4 lists analytical tools, programs, and algorithms, the second column provides brief descriptions thereof, the third column presents appropriate references, all of which are incorporated by reference herein in their entirety, and the fourth column presents, where applicable, the scores, probability values, and other parameters used to evaluate the strength of a match between two sequences (the higher the score, the greater the homology between two sequences).

DETAILED DESCRIPTION OF THE INVENTION

Before the nucleic acid sequences and methods are presented, it is to be understood that this

invention is not limited to the particular machines, methods, and materials described. Although particular embodiments are described, machines, methods, and materials similar or equivalent to these embodiments may be used to practice the invention. The preferred machines, methods, and materials set forth are not intended to limit the scope of the invention which is limited only by the appended claims.

The singular forms "a", "an", and "the" include plural reference unless the context clearly dictates otherwise. All technical and scientific terms have the meanings commonly understood by one of ordinary skill in the art. All publications are incorporated by reference for the purpose of describing and disclosing the cell lines, vectors, and methodologies which are presented and which might be used in connection with the invention. Nothing in the specification is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention.

Definitions

As used herein, the lower case "sptm" refers to a nucleic acid sequence, while the upper case "SPTM" refers to an amino acid sequence encoded by sptm. A "full-length" sptm refers to a nucleic acid sequence containing the entire coding region of a gene endogenously expressed in human tissue.

"Adjuvants" are materials such as Freund's adjuvant, mineral gels (aluminum hydroxide), and surface active substances (lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanin, and dinitrophenol) which may be administered to increase a host's immunological response.

"Allele" refers to an alternative form of a nucleic acid sequence. Alleles result from a "mutation," a change or an alternative reading of the genetic code. Any given gene may have none, one, or many allelic forms. Mutations which give rise to alleles include deletions, additions, or substitutions of nucleotides. Each of these changes may occur alone, or in combination with the others, one or more times in a given nucleic acid sequence. The present invention encompasses allelic sptm.

"Amino acid sequence" refers to a peptide, a polypeptide, or a protein of either natural or synthetic origin. The amino acid sequence is not limited to the complete, endogenous amino acid sequence and may be a fragment, epitope, variant, or derivative of a protein expressed by a nucleic acid sequence.

"Amplification" refers to the production of additional copies of a sequence and is carried out using polymerase chain reaction (PCR) technologies well known in the art.

"Antibody" refers to intact molecules as well as to fragments thereof, such as Fab, $F(ab')_2$, and Fv fragments, which are capable of binding the epitopic determinant. Antibodies that bind SPTM polypeptides can be prepared using intact polypeptides or using fragments containing small peptides of interest as the immunizing antigen. The polypeptide or peptide used to immunize an animal (e.g., a

mouse, a rat, or a rabbit) can be derived from the translation of RNA, or synthesized chemically, and can be conjugated to a carrier protein if desired. Commonly used carriers that are chemically coupled to peptides include bovine serum albumin, thyroglobulin, and keyhole limpet hemocyanin (KLH). The coupled peptide is then used to immunize the animal.

"Antisense sequence" refers to a sequence capable of specifically hybridizing to a target sequence. The antisense sequence may include DNA, RNA, or any nucleic acid mimic or analog such as peptide nucleic acid (PNA); oligonucleotides having modified backbone linkages such as phosphorothioates, methylphosphonates, or benzylphosphonates; oligonucleotides having modified sugar groups such as 2'-methoxyethyl sugars or 2'-methoxyethoxy sugars; or oligonucleotides having modified bases such as 5-methyl cytosine, 2'-deoxyuracil, or 7-deaza-2'-deoxyguanosine.

"Antisense sequence" refers to a sequence capable of specifically hybridizing to a target sequence. The antisense sequence can be DNA, RNA, or any nucleic acid mimic or analog.

"Antisense technology" refers to any technology which relies on the specific hybridization of an antisense sequence to a target sequence.

A "bin" is a portion of computer memory space used by a computer program for storage of data, and bounded in such a manner that data stored in a bin may be retrieved by the program.

"Biologically active" refers to an amino acid sequence having a structural, regulatory, or biochemical function of a naturally occurring amino acid sequence.

"Clone joining" is a process for combining gene bins based upon the bins' containing sequence information from the same clone. The sequences may assemble into a primary gene transcript as well as one or more splice variants.

"Complementary" describes the relationship between two single-stranded nucleic acid sequences that anneal by base-pairing (5'-A-G-T-3' pairs with its complement 3'-T-C-A-5').

A "component sequence" is a nucleic acid sequence selected by a computer program such as PHRED and used to assemble a consensus or template sequence from one or more component sequences.

A "consensus sequence" or "template sequence" is a nucleic acid sequence which has been assembled from overlapping sequences, using a computer program for fragment assembly such as the GELVIEW fragment assembly system (Genetics Computer Group (GCG), Madison WI) or using a relational database management system (RDMS).

"Conservative amino acid substitutions" are those substitutions that, when made, least interfere with the properties of the original protein, i.e., the structure and especially the function of the protein is conserved and not significantly changed by such substitutions. The table below shows amino acids which may be substituted for an original amino acid in a protein and which are regarded as conservative substitutions.

Original Residue	Conservative Substitution
Ala	Gly, Ser
Arg	His, Lys
Asn	Asp, Gln, His
Asp	Asn, Glu
Cys	Ala, Ser
Gln	Asn, Glu, His
Glu	Asp, Gln, His
Gly	Ala
His	Asn, Arg, Gln, Glu
Ile	Leu, Val
Leu	Ile, Val
Lys	Arg, Gln, Glu
Met	Leu, Ile
Phe	His, Met, Leu, Trp, Tyr
Ser	Cys, Thr
Thr	Ser, Val
Trp	Phe, Tyr
Tyr	His, Phe, Trp
Val	Ile, Leu, Thr

Conservative substitutions generally maintain (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a beta sheet or alpha helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain.

"Deletion" refers to a change in either a nucleic or amino acid sequence in which at least one nucleotide or amino acid residue, respectively, is absent.

"Derivative" refers to the chemical modification of a nucleic acid sequence, such as by replacement of hydrogen by an alkyl, acyl, amino, hydroxyl, or other group.

The terms "element" and "array element" refer to a polynucleotide, polypeptide, or other chemical compound having a unique and defined position on a microarray.

"E-value" refers to the statistical probability that a match between two sequences occurred by chance.

A "fragment" is a unique portion of sptm or SPTM which is identical in sequence to but shorter in length than the parent sequence. A fragment may comprise up to the entire length of the defined sequence, minus one nucleotide/amino acid residue. For example, a fragment may comprise from 10 to 1000 contiguous amino acid residues or nucleotides. A fragment used as a probe, primer, antigen, therapeutic molecule, or for other purposes, may be at least 5, 10, 15, 16, 20, 25, 30, 40, 50, 60, 75, 100, 150, 250 or at least 500 contiguous amino acid residues or nucleotides in length. Fragments may be preferentially selected from certain regions of a molecule. For example, a polypeptide fragment may comprise a certain length of contiguous amino acids selected from the first 250 or 500 amino acids (or first 25% or 50%) of a polypeptide as shown in a certain defined

sequence. Clearly these lengths are exemplary, and any length that is supported by the specification, including the Sequence Listing and the figures, may be encompassed by the present embodiments.

A fragment of sptm comprises a region of unique polynucleotide sequence that specifically identifies sptm, for example, as distinct from any other sequence in the same genome. A fragment of sptm is useful, for example, in hybridization and amplification technologies and in analogous methods that distinguish sptm from related polynucleotide sequences. The precise length of a fragment of sptm and the region of sptm to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

A fragment of SPTM is encoded by a fragment of sptm. A fragment of SPTM comprises a region of unique amino acid sequence that specifically identifies SPTM. For example, a fragment of SPTM is useful as an immunogenic peptide for the development of antibodies that specifically recognize SPTM. The precise length of a fragment of SPTM and the region of SPTM to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

A "full length" nucleotide sequence is one containing at least a start site for translation to a protein sequence, followed by an open reading frame and a stop site, and encoding a "full length" polypeptide.

"Hit" refers to a sequence whose annotation will be used to describe a given template. Criteria for selecting the top hit are as follows: if the template has one or more exact nucleic acid matches, the top hit is the exact match with highest percent identity. If the template has no exact matches but has significant protein hits, the top hit is the protein hit with the lowest E-value. If the template has no significant protein hits, but does have significant non-exact nucleotide hits, the top hit is the nucleotide hit with the lowest E-value.

"Homology" refers to sequence similarity either between a reference nucleic acid sequence and at least a fragment of an sptm or between a reference amino acid sequence and a fragment of an SPTM.

"Hybridization" refers to the process by which a strand of nucleotides anneals with a complementary strand through base pairing. Specific hybridization is an indication that two nucleic acid sequences share a high degree of identity. Specific hybridization complexes form under defined annealing conditions, and remain hybridized after the "washing" step. The defined hybridization conditions include the annealing conditions and the washing step(s), the latter of which is particularly important in determining the stringency of the hybridization process, with more stringent conditions allowing less non-specific binding, i.e., binding between pairs of nucleic acid probes that are not perfectly matched. Permissive conditions for annealing of nucleic acid sequences are routinely determinable and may be consistent among hybridization experiments, whereas wash conditions may be varied among experiments to achieve the desired stringency.

Generally, stringency of hybridization is expressed with reference to the temperature under which the wash step is carried out. Generally, such wash temperatures are selected to be about 5°C to 20°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. An equation for calculating T_m and conditions for nucleic acid hybridization is well known and can be found in Sambrook et al., 1989, Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; specifically see volume 2, chapter 9.

High stringency conditions for hybridization between polynucleotides of the present invention include wash conditions of 68°C in the presence of about 0.2 x SSC and about 0.1% SDS, for 1 hour. Alternatively, temperatures of about 65°C, 60°C, or 55°C may be used. SSC concentration may be varied from about 0.2 to 2 x SSC, with SDS being present at about 0.1%. Typically, blocking reagents are used to block non-specific hybridization. Such blocking reagents include, for instance, denatured salmon sperm DNA at about 100-200 µg/ml. Useful variations on these conditions will be readily apparent to those skilled in the art. Hybridization, particularly under high stringency conditions, may be suggestive of evolutionary similarity between the nucleotides. Such similarity is strongly indicative of a similar role for the nucleotides and their resultant proteins.

Other parameters, such as temperature, salt concentration, and detergent concentration may be varied to achieve the desired stringency. Denaturants, such as formamide at a concentration of about 35-50% v/v, may also be used under particular circumstances, such as RNA:DNA hybridizations. Appropriate hybridization conditions are routinely determinable by one of ordinary skill in the art.

"Immunogenic" describes the potential for a natural, recombinant, or synthetic peptide, epitope, polypeptide, or protein to induce antibody production in appropriate animals, cells, or cell lines.

"Insertion" or "addition" refers to a change in either a nucleic or amino acid sequence in which at least one nucleotide or residue, respectively, is added to the sequence.

"Labeling" refers to the covalent or noncovalent joining of a polynucleotide, polypeptide, or antibody with a reporter molecule capable of producing a detectable or measurable signal.

"Microarray" is any arrangement of nucleic acids, amino acids, antibodies, etc., on a substrate. The substrate may be a solid support such as beads, glass, paper, nitrocellulose, nylon, or an appropriate membrane.

"Linkers" are short stretches of nucleotide sequence which may be added to a vector or an sptm to create restriction endonuclease sites to facilitate cloning. "Polylinkers" are engineered to incorporate multiple restriction enzyme sites and to provide for the use of enzymes which leave 5' or

3' overhangs (e.g., BamHI, EcoRI, and HindIII) and those which provide blunt ends (e.g., EcoRV, SnaBI, and StuI).

"Naturally occurring" refers to an endogenous polynucleotide or polypeptide that may be isolated from viruses or prokaryotic or eukaryotic cells.

"Nucleic acid sequence" refers to the specific order of nucleotides joined by phosphodiester bonds in a linear, polymeric arrangement. Depending on the number of nucleotides, the nucleic acid sequence can be considered an oligomer, oligonucleotide, or polynucleotide. The nucleic acid can be DNA, RNA, or any nucleic acid analog, such as PNA, may be of genomic or synthetic origin, may be either double-stranded or single-stranded, and can represent either the sense or antisense (complementary) strand.

"Oligomer" refers to a nucleic acid sequence of at least about 6 nucleotides and as many as about 60 nucleotides, preferably about 15 to 40 nucleotides, and most preferably between about 20 and 30 nucleotides, that may be used in hybridization or amplification technologies. Oligomers may be used as, e.g., primers for PCR, and are usually chemically synthesized.

"Operably linked" refers to the situation in which a first nucleic acid sequence is placed in a functional relationship with the second nucleic acid sequence. For instance, a promoter is operably linked to a coding sequence if the promoter affects the transcription or expression of the coding sequence. Generally, operably linked DNA sequences may be in close proximity or contiguous and, where necessary to join two protein coding regions, in the same reading frame.

"Peptide nucleic acid" (PNA) refers to a DNA mimic in which nucleotide bases are attached to a pseudopeptide backbone to increase stability. PNAs, also designated antigene agents, can prevent gene expression by targeting complementary messenger RNA.

The phrases "percent identity" and "% identity", as applied to polynucleotide sequences, refer to the percentage of residue matches between at least two polynucleotide sequences aligned using a standardized algorithm. Such an algorithm may insert, in a standardized and reproducible way, gaps in the sequences being compared in order to optimize alignment between two sequences, and therefore achieve a more meaningful comparison of the two sequences.

Percent identity between polynucleotide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program. This program is part of the LASERGENE software package, a suite of molecular biological analysis programs (DNASTAR, Madison WI). CLUSTAL V is described in Higgins, D.G. and Sharp, P.M. (1989) CABIOS 5:151-153 and in Higgins, D.G. et al. (1992) CABIOS 8:189-191. For pairwise alignments of polynucleotide sequences, the default parameters are set as follows: Ktuple=2, gap penalty=5, window=4, and "diagonals saved"=4. The "weighted" residue weight table is selected as the default. Percent identity is reported by CLUSTAL V as the "percent similarity" between aligned polynucleotide sequence pairs.

Alternatively, a suite of commonly used and freely available sequence comparison algorithms is provided by the National Center for Biotechnology Information (NCBI) Basic Local Alignment Search Tool (BLAST) (Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410), which is available from several sources, including the NCBI, Bethesda, MD, and on the Internet at http://www.ncbi.nlm.nih.gov/BLAST/. The BLAST software suite includes various sequence analysis programs including "blastn," that is used to determine alignment between a known polynucleotide sequence and other sequences on a variety of databases. Also available is a tool called "BLAST 2 Sequences" that is used for direct pairwise comparison of two nucleotide sequences. "BLAST 2 Sequences" can be accessed and used interactively at http://www.ncbi.nlm.nih.gov/gorf/bl2/. The "BLAST 2 Sequences" tool can be used for both blastn and blastp (discussed below). BLAST programs are commonly used with gap and other parameters set to default settings. For example, to compare two nucleotide sequences, one may use blastn with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such default parameters may be, for example:

Matrix: BLOSUM62
Reward for match: 1
Penalty for mismatch: -2
Open Gap: 5 and Extension Gap: 2 penalties
Gap x drop-off: 50
Expect: 10
Word Size: 11
Filter: on

Percent identity may be measured over the length of an entire defined sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined sequence, for instance, a fragment of at least 20, at least 30, at least 40, at least 50, at least 70, at least 100, or at least 200 contiguous nucleotides. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in figures or Sequence Listings, may be used to describe a length over which percentage identity may be measured.

Nucleic acid sequences that do not show a high degree of identity may nevertheless encode similar amino acid sequences due to the degeneracy of the genetic code. It is understood that changes in nucleic acid sequence can be made using this degeneracy to produce multiple nucleic acid sequences that all encode substantially the same protein.

The phrases "percent identity" and "% identity", as applied to polypeptide sequences, refer to the percentage of residue matches between at least two polypeptide sequences aligned using a standardized algorithm. Methods of polypeptide sequence alignment are well-known. Some

alignment methods take into account conservative amino acid substitutions. Such conservative substitutions, explained in more detail above, generally preserve the hydrophobicity and acidity of the substituted residue, thus preserving the structure (and therefore function) of the folded polypeptide.

Percent identity between polypeptide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program (described and referenced above). For pairwise alignments of polypeptide sequences using CLUSTAL V, the default parameters are set as follows: Ktuple=1, gap penalty=3, window=5, and "diagonals saved"=5. The PAM250 matrix is selected as the default residue weight table. As with polynucleotide alignments, the percent identity is reported by CLUSTAL V as the "percent similarity" between aligned polypeptide sequence pairs.

Alternatively the NCBI BLAST software suite may be used. For example, for a pairwise comparison of two polypeptide sequences, one may use the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) with blastp set at default parameters. Such default parameters may be, for example:

Matrix: BLOSUM62

Open Gap: 11 and Extension Gap: 1 penalty

Gap x drop-off: 50

Expect: 10

Word Size: 3

Filter: on

Percent identity may be measured over the length of an entire defined polypeptide sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined polypeptide sequence, for instance, a fragment of at least 15, at least 20, at least 30, at least 40, at least 50, at least 70 or at least 150 contiguous residues. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in figures or Sequence Listings, may be used to describe a length over which percentage identity may be measured.

"Post-translational modification" of an SPTM may involve lipidation, glycosylation, phosphorylation, acetylation, racemization, proteolytic cleavage, and other modifications known in the art. These processes may occur synthetically or biochemically. Biochemical modifications will vary by cell type depending on the enzymatic milieu and the SPTM.

"Probe" refers to sptm or fragments thereof, which are used to detect identical, allelic or related nucleic acid sequences. Probes are isolated oligonucleotides or polynucleotides attached to a detectable label or reporter molecule. Typical labels include radioactive isotopes, ligands, chemiluminescent agents, and enzymes. "Primers" are short nucleic acids, usually DNA oligonucleotides, which may be annealed to a target polynucleotide by complementary base-pairing. The primer may then be extended along the target DNA strand by a DNA polymerase enzyme.

Primer pairs can be used for amplification (and identification) of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR).

Probes and primers as used in the present invention typically comprise at least 15 contiguous nucleotides of a known sequence. In order to enhance specificity, longer probes and primers may also be employed, such as probes and primers that comprise at least 20, 30, 40, 50, 60, 70, 80, 90, 100, or at least 150 consecutive nucleotides of the disclosed nucleic acid sequences. Probes and primers may be considerably longer than these examples, and it is understood that any length supported by the specification, including the figures and Sequence Listing, may be used.

Methods for preparing and using probes and primers are described in the references, for example Sambrook et al., 1989, Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; Ausubel et al.,1987, Current Protocols in Molecular Biology, Greene Publ. Assoc. & Wiley-Intersciences, New York NY; Innis et al., 1990, PCR Protocols, A Guide to Methods and Applications, Academic Press, San Diego CA. PCR primer pairs can be derived from a known sequence, for example, by using computer programs intended for that purpose such as Primer (Version 0.5, 1991, Whitehead Institute for Biomedical Research, Cambridge MA).

Oligonucleotides for use as primers are selected using software known in the art for such purpose. For example, OLIGO 4.06 software is useful for the selection of PCR primer pairs of up to 100 nucleotides each, and for the analysis of oligonucleotides and larger polynucleotides of up to 5,000 nucleotides from an input polynucleotide sequence of up to 32 kilobases. Similar primer selection programs have incorporated additional features for expanded capabilities. For example, the PrimOU primer selection program (available to the public from the Genome Center at University of Texas South West Medical Center, Dallas TX) is capable of choosing specific primers from megabase sequences and is thus useful for designing primers on a genome-wide scope. The Primer3 primer selection program (available to the public from the Whitehead Institute/MIT Center for Genome Research, Cambridge MA) allows the user to input a "mispriming library," in which sequences to avoid as primer binding sites are user-specified. Primer3 is useful, in particular, for the selection of oligonucleotides for microarrays. (The source code for the latter two primer selection programs may also be obtained from their respective sources and modified to meet the user's specific needs.) The PrimeGen program (available to the public from the UK Human Genome Mapping Project Resource Centre, Cambridge UK) designs primers based on multiple sequence alignments, thereby allowing selection of primers that hybridize to either the most conserved or least conserved regions of aligned nucleic acid sequences. Hence, this program is useful for identification of both unique and conserved oligonucleotides and polynucleotide fragments. The oligonucleotides and polynucleotide fragments identified by any of the above selection methods are useful in hybridization technologies, for example, as PCR or sequencing primers, microarray elements, or specific probes to

identify fully or partially complementary polynucleotides in a sample of nucleic acids. Methods of oligonucleotide selection are not limited to those described above.

"Purified" refers to molecules, either polynucleotides or polypeptides that are isolated or separated from their natural environment and are at least 60% free, preferably at least 75% free, and most preferably at least 90% free from other compounds with which they are naturally associated.

A "recombinant nucleic acid" is a sequence that is not naturally occurring or has a sequence that is made by an artificial combination of two or more otherwise separated segments of sequence. This artificial combination is often accomplished by chemical synthesis or, more commonly, by the artificial manipulation of isolated segments of nucleic acids, e.g., by genetic engineering techniques such as those described in Sambrook, supra. The term recombinant includes nucleic acids that have been altered solely by addition, substitution, or deletion of a portion of the nucleic acid. Frequently, a recombinant nucleic acid may include a nucleic acid sequence operably linked to a promoter sequence. Such a recombinant nucleic acid may be part of a vector that is used, for example, to transform a cell.

Alternatively, such recombinant nucleic acids may be part of a viral vector, e.g., based on a vaccinia virus, that could be use to vaccinate a mammal wherein the recombinant nucleic acid is expressed, inducing a protective immunological response in the mammal.

"Regulatory element" refers to a nucleic acid sequence from nontranslated regions of a gene, and includes enhancers, promoters, introns, and 3' untranslated regions, which interact with host proteins to carry out or regulate transcription or translation.

"Reporter" molecules are chemical or biochemical moieties used for labeling a nucleic acid, an amino acid, or an antibody. They include radionuclides; enzymes; fluorescent, chemiluminescent, or chromogenic agents; substrates; cofactors; inhibitors; magnetic particles; and other moieties known in the art.

An "RNA equivalent," in reference to a DNA sequence, is composed of the same linear sequence of nucleotides as the reference DNA sequence with the exception that all occurrences of the nitrogenous base thymine are replaced with uracil, and the sugar backbone is composed of ribose instead of deoxyribose.

"Sample" is used in its broadest sense. Samples may contain nucleic or amino acids, antibodies, or other materials, and may be derived from any source (e.g., bodily fluids including, but not limited to, saliva, blood, and urine; chromosome(s), organelles, or membranes isolated from a cell; genomic DNA, RNA, or cDNA in solution or bound to a substrate; and cleared cells or tissues or blots or imprints from such cells or tissues).

"Specific binding" or "specifically binding" refers to the interaction between a protein or peptide and its agonist, antibody, antagonist, or other binding partner. The interaction is dependent upon the presence of a particular structure of the protein, e.g., the antigenic determinant or epitope,

recognized by the binding molecule. For example, if an antibody is specific for epitope "A," the presence of a polypeptide containing epitope A, or the presence of free unlabeled A, in a reaction containing free labeled A and the antibody will reduce the amount of labeled A that binds to the antibody.

"Substitution" refers to the replacement of at least one nucleotide or amino acid by a different nucleotide or amino acid.

"Substrate" refers to any suitable rigid or semi-rigid support including, e.g., membranes, filters, chips, slides, wafers, fibers, magnetic or nonmagnetic beads, gels, tubing, plates, polymers, microparticles or capillaries. The substrate can have a variety of surface forms, such as wells, trenches, pins, channels and pores, to which polynucleotides or polypeptides are bound.

A "transcript image" refers to the collective pattern of gene expression by a particular tissue or cell type under given conditions at a given time.

"Transformation" refers to a process by which exogenous DNA enters a recipient cell. Transformation may occur under natural or artificial conditions using various methods well known in the art. Transformation may rely on any known method for the insertion of foreign nucleic acid sequences into a prokaryotic or eukaryotic host cell. The method is selected based on the host cell being transformed.

"Transformants" include stably transformed cells in which the inserted DNA is capable of replication either as an autonomously replicating plasmid or as part of the host chromosome, as well as cells which transiently express inserted DNA or RNA.

A "transgenic organism," as used herein, is any organism, including but not limited to animals and plants, in which one or more of the cells of the organism contains heterologous nucleic acid introduced by way of human intervention, such as by transgenic techniques well known in the art. The nucleic acid is introduced into the cell, directly or indirectly by introduction into a precursor of the cell, by way of deliberate genetic manipulation, such as by microinjection or by infection with a recombinant virus. The term genetic manipulation does not include classical cross-breeding, or in vitro fertilization, but rather is directed to the introduction of a recombinant DNA molecule. The transgenic organisms contemplated in accordance with the present invention include bacteria, cyanobacteria, fungi, and plants and animals. The isolated DNA of the present invention can be introduced into the host by methods known in the art, for example infection, transfection, transformation or transconjugation. Techniques for transferring the DNA of the present invention into such organisms are widely known and provided in references such as Sambrook et al. (1989), supra.

A "variant" of a particular nucleic acid sequence is defined as a nucleic acid sequence having at least 25% sequence identity to the particular nucleic acid sequence over a certain length of one of the nucleic acid sequences using blastn with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-

1999) set at default parameters. Such a pair of nucleic acids may show, for example, at least 30%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% or even at least 98% or greater sequence identity over a certain defined length. The variant may result in "conservative" amino acid changes which do not affect structural and/or chemical properties. A variant may be described as, for example, an "allelic" (as defined above), "splice," "species," or "polymorphic" variant. A splice variant may have significant identity to a reference molecule, but will generally have a greater or lesser number of polynucleotides due to alternate splicing of exons during mRNA processing. The corresponding polypeptide may possess additional functional domains or lack domains that are present in the reference molecule. Species variants are polynucleotide sequences that vary from one species to another. The resulting polypeptides generally will have significant amino acid identity relative to each other. A polymorphic variant is a variation in the polynucleotide sequence of a particular gene between individuals of a given species. Polymorphic variants also may encompass "single nucleotide polymorphisms" (SNPs) in which the polynucleotide sequence varies by one base. The presence of SNPs may be indicative of, for example, a certain population, a disease state, or a propensity for a disease state.

In an alternative, variants of the polynucleotides of the present invention may be generated through recombinant methods. One possible method is a DNA shuffling technique such as MOLECULARBREEDING (Maxygen Inc., Santa Clara CA; described in U.S. Patent Number 5,837,458; Chang, C.-C. et al. (1999) Nat. Biotechnol. 17:793-797; Christians, F.C. et al. (1999) Nat. Biotechnol. 17:259-264; and Crameri, A. et al. (1996) Nat. Biotechnol. 14:315-319) to alter or improve the biological properties of SPTM, such as its biological or enzymatic activity or its ability to bind to other molecules or compounds. DNA shuffling is a process by which a library of gene variants is produced using PCR-mediated recombination of gene fragments. The library is then subjected to selection or screening procedures that identify those gene variants with the desired properties. These preferred variants may then be pooled and further subjected to recursive rounds of DNA shuffling and selection/screening. Thus, genetic diversity is created through "artificial" breeding and rapid molecular evolution. For example, fragments of a single gene containing random point mutations may be recombined, screened, and then reshuffled until the desired properties are optimized. Alternatively, fragments of a given gene may be recombined with fragments of homologous genes in the same gene family, either from the same or different species, thereby maximizing the genetic diversity of multiple naturally occurring genes in a directed and controllable manner.

A "variant" of a particular polypeptide sequence is defined as a polypeptide sequence having at least 40% sequence identity to the particular polypeptide sequence over a certain length of one of the polypeptide sequences using blastp with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such a pair of polypeptides may show, for example, at least 50%, at

least 60%, at least 70%, at least 80%, at least 90%, at least 95%, or at least 98% or greater sequence identity over a certain defined length of one of the polypeptides.

THE INVENTION

In a particular embodiment, cDNA sequences derived from human tissues and cell lines were aligned based on nucleotide sequence identity and assembled into "consensus" or "template" sequences which are designated by the template identification numbers (template IDs) in column 2 of Table 1. The sequence identification numbers (SEQ ID NO:s) corresponding to the template IDs are shown in column 1. The template sequences have similarity to GenBank sequences, or "hits," as designated by the GI Numbers in column 3. The statistical probability of each GenBank hit is indicated by a probability score in column 4, and the functional annotation corresponding to each GenBank hit is listed in column 5.

Segments of each template sequences are defined by the "start" and "stop" nucleotide positions listed in columns 3 and 4 of Table 2. These segments, when translated in the reading frames indicated in column 5, have similarity to signal peptide (SP) or transmembrane (TM) domain consensus sequences, as indicated in column 6.

The invention incorporates the nucleic acid sequences of these templates as disclosed in the Sequence Listing and the use of these sequences in the diagnosis and treatment of disease states characterized by defects in cell signaling. The invention further utilizes these sequences in hybridization and amplification technologies, and in particular, in technologies which assess gene expression patterns correlated with specific cells or tissues and their responses in vivo or in vitro to pharmaceutical agents, toxins, and other treatments. In this manner, the sequences of the present invention are used to develop a transcript image for a particular cell or tissue.

Derivation of Nucleic Acid Sequences

cDNA was isolated from libraries constructed using RNA derived from normal and diseased human tissues and cell lines. The human tissues and cell lines used for cDNA library construction were selected from a broad range of sources to provide a diverse population of cDNAs representative of gene transcription throughout the human body. Descriptions of the human tissues and cell lines used for cDNA library construction are provided in the LIFESEQ database (Incyte Genomics, Inc. (Incyte), Palo Alto CA). Human tissues were broadly selected from, for example, cardiovascular, dermatologic, endocrine, gastrointestinal, hematopoietic/immune system, musculoskeletal, neural, reproductive, and urologic sources.

Cell lines used for cDNA library construction were derived from, for example, leukemic cells, teratocarcinomas, neuroepitheliomas, cervical carcinoma, lung fibroblasts, and endothelial cells. Such cell lines include, for example, THP-1, Jurkat, HUVEC, hNT2, WI38, HeLa, and other cell

lines commonly used and available from public depositories (American Type Culture Collection, Manassas VA). Prior to mRNA isolation, cell lines were untreated, treated with a pharmaceutical agent such as 5'-aza-2'-deoxycytidine, treated with an activating agent such as lipopolysaccharide in the case of leukocytic cell lines, or, in the case of endothelial cell lines, subjected to shear stress.

Sequencing of the cDNAs

Methods for DNA sequencing are well known in the art. Conventional enzymatic methods employ the Klenow fragment of DNA polymerase I, SEQUENASE DNA polymerase (U.S. Biochemical Corporation, Cleveland OH), Taq polymerase (PE Biosystems, Foster City CA), thermostable T7 polymerase (Amersham Pharmacia Biotech, Inc. (Amersham Pharmacia Biotech), Piscataway NJ), or combinations of polymerases and proofreading exonucleases such as those found in the ELONGASE amplification system (Life Technologies Inc. (Life Technologies), Gaithersburg MD), to extend the nucleic acid sequence from an oligonucleotide primer annealed to the DNA template of interest. Methods have been developed for the use of both single-stranded and double-stranded templates. Chain termination reaction products may be electrophoresed on urea-polyacrylamide gels and detected either by autoradiography (for radioisotope-labeled nucleotides) or by fluorescence (for fluorophore-labeled nucleotides). Automated methods for mechanized reaction preparation, sequencing, and analysis using fluorescence detection methods have been developed. Machines used to prepare cDNAs for sequencing can include the MICROLAB 2200 liquid transfer system (Hamilton Company (Hamilton), Reno NV), Peltier thermal cycler (PTC200; MJ Research, Inc. (MJ Research), Watertown MA), and ABI CATALYST 800 thermal cycler (PE Biosystems). Sequencing can be carried out using, for example, the ABI 373 or 377 (PE Biosystems) or MEGABACE 1000 (Molecular Dynamics, Inc. (Molecular Dynamics), Sunnyvale CA) DNA sequencing systems, or other automated and manual sequencing systems well known in the art.

The nucleotide sequences of the Sequence Listing have been prepared by current, state-of-the-art, automated methods and, as such, may contain occasional sequencing errors or unidentified nucleotides. Such unidentified nucleotides are designated by an N. These infrequent unidentified bases do not represent a hindrance to practicing the invention for those skilled in the art. Several methods employing standard recombinant techniques may be used to correct errors and complete the missing sequence information. (See, e.g., those described in Ausubel, F.M. et al. (1997) Short Protocols in Molecular Biology, John Wiley & Sons, New York NY; and Sambrook, J. et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview NY.)

Assembly of cDNA Sequences

Human polynucleotide sequences may be assembled using programs or algorithms well known in the art. Sequences to be assembled are related, wholly or in part, and may be derived from

a single or many different transcripts. Assembly of the sequences can be performed using such programs as PHRAP (Phils Revised Assembly Program) and the GELVIEW fragment assembly system (GCG), or other methods known in the art.

Alternatively, cDNA sequences are used as "component" sequences that are assembled into "template" or "consensus" sequences as follows. Sequence chromatograms are processed, verified, and quality scores are obtained using PHRED. Raw sequences are edited using an editing pathway known as Block 1 (See, e.g., the LIFESEQ Assembled User Guide, Incyte Genomics, Palo Alto, CA). A series of BLAST comparisons is performed and low-information segments and repetitive elements (e.g., dinucleotide repeats, Alu repeats, etc.) are replaced by "n's", or masked, to prevent spurious matches. Mitochondrial and ribosomal RNA sequences are also removed. The processed sequences are then loaded into a relational database management system (RDMS) which assigns edited sequences to existing templates, if available. When additional sequences are added into the RDMS, a process is initiated which modifies existing templates or creates new templates from works in progress (i.e., nonfinal assembled sequences) containing queued sequences or the sequences themselves. After the new sequences have been assigned to templates, the templates can be merged into bins. If multiple templates exist in one bin, the bin can be split and the templates reannotated.

Once gene bins have been generated based upon sequence alignments, bins are "clone joined" based upon clone information. Clone joining occurs when the 5' sequence of one clone is present in one bin and the 3' sequence from the same clone is present in a different bin, indicating that the two bins should be merged into a single bin. Only bins which share at least two different clones are merged.

A resultant template sequence may contain either a partial or a full length open reading frame, or all or part of a genetic regulatory element. This variation is due in part to the fact that the full length cDNAs of many genes are several hundred, and sometimes several thousand, bases in length. With current technology, cDNAs comprising the coding regions of large genes cannot be cloned because of vector limitations, incomplete reverse transcription of the mRNA, or incomplete "second strand" synthesis. Template sequences may be extended to include additional contiguous sequences derived from the parent RNA transcript using a variety of methods known to those of skill in the art. Extension may thus be used to achieve the full length coding sequence of a gene.

Analysis of the cDNA Sequences

The cDNA sequences are analyzed using a variety of programs and algorithms which are well known in the art. (See, e.g., Ausubel, 1997, supra, Chapter 7.7; Meyers, R.A. (Ed.) (1995) Molecular Biology and Biotechnology, Wiley VCH, New York NY, pp. 856-853; and Table 4.) These analyses comprise both reading frame determinations, e.g., based on triplet codon periodicity for particular

organisms (Fickett, J.W. (1982) Nucleic Acids Res. 10:5303-5318); analyses of potential start and stop codons; and homology searches.

Computer programs known to those of skill in the art for performing computer-assisted searches for amino acid and nucleic acid sequence similarity, include, for example, Basic Local Alignment Search Tool (BLAST; Altschul, S.F. (1993) J. Mol. Evol. 36:290-300; Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410). BLAST is especially useful in determining exact matches and comparing two sequence fragments of arbitrary but equal lengths, whose alignment is locally maximal and for which the alignment score meets or exceeds a threshold or cutoff score set by the user (Karlin, S. et al. (1988) Proc. Natl. Acad. Sci. USA 85:841-845). Using an appropriate search tool (e.g., BLAST or HMM), GenBank, SwissProt, BLOCKS, PFAM and other databases may be searched for sequences containing regions of homology to a query sptm or SPTM of the present invention.

Other approaches to the identification, assembly, storage, and display of nucleotide and polypeptide sequences are provided in "Relational Database for Storing Biomolecule Information," U.S.S.N. 08/947,845, filed October 9, 1997; "Project-Based Full-Length Biomolecular Sequence Database," U.S.S.N. 08/811,758, filed March 6, 1997; and "Relational Database and System for Storing Information Relating to Biomolecular Sequences," U.S.S.N. 09/034,807, filed March 4, 1998, all of which are incorporated by reference herein in their entirety.

Protein hierarchies can be assigned to the putative encoded polypeptide based on, e.g., motif, BLAST, or biological analysis. Methods for assigning these hierarchies are described, for example, in "Database System Employing Protein Function Hierarchies for Viewing Biomolecular Sequence Data," U.S.S.N. 08/812,290, filed March 6, 1997, incorporated herein by reference.

Sequences of Human Secretory Molecules

The sptm of the present invention may be used for a variety of diagnostic and therapeutic purposes. For example, an sptm may be used to diagnose a particular condition, disease, or disorder associated with cell signaling. Such conditions, diseases, and disorders include, but are not limited to, a cell proliferative disorder such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, a cancer of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus; an immune system disorder such as such as inflammation, actinic keratosis, acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis,

amyloidosis, anemia, arteriosclerosis, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, bronchitis, bursitis, cholecystitis, cirrhosis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, paroxysmal nocturnal hemoglobinuria, hepatitis, hypereosinophilia, irritable bowel syndrome, episodic lymphopenia with lymphocytotoxins, mixed connective tissue disease (MCTD), multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, myelofibrosis, osteoarthritis, osteoporosis, pancreatitis, polycythemia vera, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, primary thrombocythemia, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, trauma, and hematopoietic cancer including lymphoma, leukemia, and myeloma; and a neurological disorder such as epilepsy, ischemic cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's disease, Pick's disease, Huntington's disease, dementia, Parkinson's disease and other extrapyramidal disorders, amyotrophic lateral sclerosis and other motor neuron disorders, progressive neural muscular atrophy, retinitis pigmentosa, hereditary ataxias, multiple sclerosis and other demyelinating diseases, bacterial and viral meningitis, brain abscess, subdural empyema, epidural abscess, suppurative intracranial thrombophlebitis, myelitis and radiculitis, viral central nervous system disease, prion diseases including kuru, Creutzfeldt-Jakob disease, and Gerstmann-Straussler-Scheinker syndrome, fatal familial insomnia, nutritional and metabolic diseases of the nervous system, neurofibromatosis, tuberous sclerosis, cerebelloretinal hemangioblastomatosis, encephalotrigeminal syndrome, mental retardation and other developmental disorder of the central nervous system, cerebral palsy, a neuroskeletal disorder, an autonomic nervous system disorder, a cranial nerve disorder, a spinal cord disease, muscular dystrophy and other neuromuscular disorder, a peripheral nervous system disorder, dermatomyositis and polymyositis, inherited, metabolic, endocrine, and toxic myopathy, myasthenia gravis, periodic paralysis, a mental disorder including mood, anxiety, and schizophrenic disorder, seasonal affective disorder (SAD), akathesia, amnesia, catatonia, diabetic neuropathy, tardive dyskinesia, dystonias, paranoid psychoses, postherpetic neuralgia, and Tourette's disorder. The sptm can be used to detect the presence of, or to quantify the amount of, an sptm-related polynucleotide in a sample. This information is then compared to information obtained from appropriate reference samples, and a diagnosis is established. Alternatively, a polynucleotide complementary to a given sptm can inhibit or inactivate a therapeutically relevant gene related to the sptm.

Analysis of sptm Expression Patterns

The expression of sptm may be routinely assessed by hybridization-based methods to determine, for example, the tissue-specificity, disease-specificity, or developmental stage-specificity of sptm expression. For example, the level of expression of sptm may be compared among different cell types or tissues, among diseased and normal cell types or tissues, among cell types or tissues at different developmental stages, or among cell types or tissues undergoing various treatments. This type of analysis is useful, for example, to assess the relative levels of sptm expression in fully or partially differentiated cells or tissues, to determine if changes in sptm expression levels are correlated with the development or progression of specific disease states, and to assess the response of a cell or tissue to a specific therapy, for example, in pharmacological or toxicological studies. Methods for the analysis of sptm expression are based on hybridization and amplification technologies and include membrane-based procedures such as northern blot analysis, high-throughput procedures that utilize, for example, microarrays, and PCR-based procedures.

Hybridization and Genetic Analysis

The sptm, their fragments, or complementary sequences, may be used to identify the presence of and/or to determine the degree of similarity between two (or more) nucleic acid sequences. The sptm may be hybridized to naturally occurring or recombinant nucleic acid sequences under appropriately selected temperatures and salt concentrations. Hybridization with a probe based on the nucleic acid sequence of at least one of the sptm allows for the detection of nucleic acid sequences, including genomic sequences, which are identical or related to the sptm of the Sequence Listing. Probes may be selected from non-conserved or unique regions of at least one of the polynucleotides of SEQ ID NO:1-26 and tested for their ability to identify or amplify the target nucleic acid sequence using standard protocols.

Polynucleotide sequences that are capable of hybridizing, in particular, to those shown in SEQ ID NO:1-26 and fragments thereof, can be identified using various conditions of stringency. (See, e.g., Wahl, G.M. and S.L. Berger (1987) Methods Enzymol. 152:399-407; Kimmel, A.R. (1987) Methods Enzymol. 152:507-511.) Hybridization conditions are discussed in "Definitions."

A probe for use in Southern or northern hybridization may be derived from a fragment of an sptm sequence, or its complement, that is up to several hundred nucleotides in length and is either single-stranded or double-stranded. Such probes may be hybridized in solution to biological materials such as plasmids, bacterial, yeast, or human artificial chromosomes, cleared or sectioned tissues, or to artificial substrates containing sptm. Microarrays are particularly suitable for identifying the presence of and detecting the level of expression for multiple genes of interest by examining gene expression correlated with, e.g., various stages of development, treatment with a drug or compound, or disease progression. An array analogous to a dot or slot blot may be used to arrange and link

polynucleotides to the surface of a substrate using one or more of the following: mechanical (vacuum), chemical, thermal, or UV bonding procedures. Such an array may contain any number of sptm and may be produced by hand or by using available devices, materials, and machines.

Microarrays may be prepared, used, and analyzed using methods known in the art. (See, e.g., Brennan, T.M. et al. (1995) U.S. Patent No. 5,474,796; Schena, M. et al. (1996) Proc. Natl. Acad. Sci. USA 93:10614-10619; Baldeschweiler et al. (1995) PCT application WO95/251116; Shalon, D. et al. (1995) PCT application WO95/35505; Heller, R.A. et al. (1997) Proc. Natl. Acad. Sci. USA 94:2150-2155; and Heller, M.J. et al. (1997) U.S. Patent No. 5,605,662.)

Probes may be labeled by either PCR or enzymatic techniques using a variety of commercially available reporter molecules. For example, commercial kits are available for radioactive and chemiluminescent labeling (Amersham Pharmacia Biotech) and for alkaline phosphatase labeling (Life Technologies). Alternatively, sptm may be cloned into commercially available vectors for the production of RNA probes. Such probes may be transcribed in the presence of at least one labeled nucleotide (e.g., ^{32}P-ATP, Amersham Pharmacia Biotech).

Additionally the polynucleotides of SEQ ID NO:1-26 or suitable fragments thereof can be used to isolate full length cDNA sequences utilizing hybridization and/or amplification procedures well known in the art, e.g., cDNA library screening, PCR amplification, etc. The molecular cloning of such full length cDNA sequences may employ the method of cDNA library screening with probes using the hybridization, stringency, washing, and probing strategies described above and in Ausubel, supra, Chapters 3, 5, and 6. These procedures may also be employed with genomic libraries to isolate genomic sequences of sptm in order to analyze, e.g., regulatory elements.

Genetic Mapping

Gene identification and mapping are important in the investigation and treatment of almost all conditions, diseases, and disorders. Cancer, cardiovascular disease, Alzheimer's disease, arthritis, diabetes, and mental illnesses are of particular interest. Each of these conditions is more complex than the single gene defects of sickle cell anemia or cystic fibrosis, with select groups of genes being predictive of predisposition for a particular condition, disease, or disorder. For example, cardiovascular disease may result from malfunctioning receptor molecules that fail to clear cholesterol from the bloodstream, and diabetes may result when a particular individual's immune system is activated by an infection and attacks the insulin-producing cells of the pancreas. In some studies, Alzheimer's disease has been linked to a gene on chromosome 21; other studies predict a different gene and location. Mapping of disease genes is a complex and reiterative process and generally proceeds from genetic linkage analysis to physical mapping.

As a condition is noted among members of a family, a genetic linkage map traces parts of chromosomes that are inherited in the same pattern as the condition. Statistics link the inheritance of

particular conditions to particular regions of chromosomes, as defined by RFLP or other markers. (See, for example, Lander, E. S. and Botstein, D. (1986) Proc. Natl. Acad. Sci. USA 83:7353-7357.) Occasionally, genetic markers and their locations are known from previous studies. More often, however, the markers are simply stretches of DNA that differ among individuals. Examples of genetic linkage maps can be found in various scientific journals or at the Online Mendelian Inheritance in Man (OMIM) World Wide Web site.

In another embodiment of the invention, sptm sequences may be used to generate hybridization probes useful in chromosomal mapping of naturally occurring genomic sequences. Either coding or noncoding sequences of sptm may be used, and in some instances, noncoding sequences may be preferable over coding sequences. For example, conservation of an sptm coding sequence among members of a multi-gene family may potentially cause undesired cross hybridization during chromosomal mapping. The sequences may be mapped to a particular chromosome, to a specific region of a chromosome, or to artificial chromosome constructions, e.g., human artificial chromosomes (HACs), yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), bacterial P1 constructions, or single chromosome cDNA libraries. (See, e.g., Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355; Price, C.M. (1993) Blood Rev. 7:127-134; and Trask, B.J. (1991) Trends Genet. 7:149-154.)

Fluorescent in situ hybridization (FISH) may be correlated with other physical chromosome mapping techniques and genetic map data. (See, e.g., Meyers, supra, pp. 965-968.) Correlation between the location of sptm on a physical chromosomal map and a specific disorder, or a predisposition to a specific disorder, may help define the region of DNA associated with that disorder. The sptm sequences may also be used to detect polymorphisms that are genetically linked to the inheritance of a particular condition, disease, or disorder.

In situ hybridization of chromosomal preparations and genetic mapping techniques, such as linkage analysis using established chromosomal markers, may be used for extending existing genetic maps. Often the placement of a gene on the chromosome of another mammalian species, such as mouse, may reveal associated markers even if the number or arm of the corresponding human chromosome is not known. These new marker sequences can be mapped to human chromosomes and may provide valuable information to investigators searching for disease genes using positional cloning or other gene discovery techniques. Once a disease or syndrome has been crudely correlated by genetic linkage with a particular genomic region, e.g., ataxia-telangiectasia to 11q22-23, any sequences mapping to that area may represent associated or regulatory genes for further investigation. (See, e.g., Gatti, R.A. et al. (1988) Nature 336:577-580.) The nucleotide sequences of the subject invention may also be used to detect differences in chromosomal architecture due to translocation, inversion, etc., among normal, carrier, or affected individuals.

Once a disease-associated gene is mapped to a chromosomal region, the gene must be cloned in order to identify mutations or other alterations (e.g., translocations or inversions) that may be correlated with disease. This process requires a physical map of the chromosomal region containing the disease-gene of interest along with associated markers. A physical map is necessary for determining the nucleotide sequence of and order of marker genes on a particular chromosomal region. Physical mapping techniques are well known in the art and require the generation of overlapping sets of cloned DNA fragments from a particular organelle, chromosome, or genome. These clones are analyzed to reconstruct and catalog their order. Once the position of a marker is determined, the DNA from that region is obtained by consulting the catalog and selecting clones from that region. The gene of interest is located through positional cloning techniques using hybridization or similar methods.

Diagnostic Uses

The sptm of the present invention may be used to design probes useful in diagnostic assays. Such assays, well known to those skilled in the art, may be used to detect or confirm conditions, disorders, or diseases associated with abnormal levels of sptm expression. Labeled probes developed from sptm sequences are added to a sample under hybridizing conditions of desired stringency. In some instances, sptm, or fragments or oligonucleotides derived from sptm, may be used as primers in amplification steps prior to hybridization. The amount of hybridization complex formed is quantified and compared with standards for that cell or tissue. If sptm expression varies significantly from the standard, the assay indicates the presence of the condition, disorder, or disease. Qualitative or quantitative diagnostic methods may include northern, dot blot, or other membrane or dip-stick based technologies or multiple-sample format technologies such as PCR, enzyme-linked immunosorbent assay (ELISA)-like, pin, or chip-based assays.

The probes described above may also be used to monitor the progress of conditions, disorders, or diseases associated with abnormal levels of sptm expression, or to evaluate the efficacy of a particular therapeutic treatment. The candidate probe may be identified from the sptm that are specific to a given human tissue and have not been observed in GenBank or other genome databases. Such a probe may be used in animal studies, preclinical tests, clinical trials, or in monitoring the treatment of an individual patient. In a typical process, standard expression is established by methods well known in the art for use as a basis of comparison, samples from patients affected by the disorder or disease are combined with the probe to evaluate any deviation from the standard profile, and a therapeutic agent is administered and effects are monitored to generate a treatment profile. Efficacy is evaluated by determining whether the expression progresses toward or returns to the standard normal pattern. Treatment profiles may be generated over a period of several days or several months.

Statistical methods well known to those skilled in the art may be use to determine the significance of such therapeutic agents.

The polynucleotides are also useful for identifying individuals from minute biological samples, for example, by matching the RFLP pattern of a sample's DNA to that of an individual's DNA. The polynucleotides of the present invention can also be used to determine the actual base-by-base DNA sequence of selected portions of an individual's genome. These sequences can be used to prepare PCR primers for amplifying and isolating such selected DNA, which can then be sequenced. Using this technique, an individual can be identified through a unique set of DNA sequences. Once a unique ID database is established for an individual, positive identification of that individual can be made from extremely small tissue samples.

In a particular aspect, oligonucleotide primers derived from the sptm of the invention may be used to detect single nucleotide polymorphisms (SNPs). SNPs are substitutions, insertions and deletions that are a frequent cause of inherited or acquired genetic disease in humans. Methods of SNP detection include, but are not limited to, single-stranded conformation polymorphism (SSCP) and fluorescent SSCP (fSSCP) methods. In SSCP, oligonucleotide primers derived from sptm are used to amplify DNA using the polymerase chain reaction (PCR). The DNA may be derived, for example, from diseased or normal tissue, biopsy samples, bodily fluids, and the like. SNPs in the DNA cause differences in the secondary and tertiary structures of PCR products in single-stranded form, and these differences are detectable using gel electrophoresis in non-denaturing gels. In fSCCP, the oligonucleotide primers are fluorescently labeled, which allows detection of the amplimers in high-throughput equipment such as DNA sequencing machines. Additionally, sequence database analysis methods, termed in silico SNP (isSNP), are capable of identifying polymorphisms by comparing the sequences of individual overlapping DNA fragments which assemble into a common consensus sequence. These computer-based methods filter out sequence variations due to laboratory preparation of DNA and sequencing errors using statistical models and automated analyses of DNA sequence chromatograms. In the alternative, SNPs may be detected and characterized by mass spectrometry using, for example, the high throughput MASSARRAY system (Sequenom, Inc., San Diego CA).

DNA-based identification techniques are critical in forensic technology. DNA sequences taken from very small biological samples such as tissues, e.g., hair or skin, or body fluids, e.g., blood, saliva, semen, etc., can be amplified using, e.g., PCR, to identify individuals. (See, e.g., Erlich, H. (1992) PCR Technology, Freeman and Co., New York, NY). Similarly, polynucleotides of the present invention can be used as polymorphic markers.

There is also a need for reagents capable of identifying the source of a particular tissue. Appropriate reagents can comprise, for example, DNA probes or primers prepared from the sequences of the present invention that are specific for particular tissues. Panels of such reagents can

identify tissue by species and/or by organ type. In a similar fashion, these reagents can be used to screen tissue cultures for contamination.

The polynucleotides of the present invention can also be used as molecular weight markers on nucleic acid gels or Southern blots, as diagnostic probes for the presence of a specific mRNA in a particular cell type, in the creation of subtracted cDNA libraries which aid in the discovery of novel polynucleotides, in selection and synthesis of oligomers for attachment to an array or other support, and as an antigen to elicit an immune response.

Disease Model Systems Using sptm

The sptm of the invention or their mammalian homologs may be "knocked out" in an animal model system using homologous recombination in embryonic stem (ES) cells. Such techniques are well known in the art and are useful for the generation of animal models of human disease. (See, e.g., U.S. Patent Number 5,175,383 and U.S. Patent Number 5,767,337.) For example, mouse ES cells, such as the mouse 129/SvJ cell line, are derived from the early mouse embryo and grown in culture. The ES cells are transformed with a vector containing the gene of interest disrupted by a marker gene, e.g., the neomycin phosphotransferase gene (neo; Capecchi, M.R. (1989) Science 244:1288-1292). The vector integrates into the corresponding region of the host genome by homologous recombination. Alternatively, homologous recombination takes place using the Cre-loxP system to knockout a gene of interest in a tissue- or developmental stage-specific manner (Marth, J.D. (1996) Clin. Invest. 97:1999-2002; Wagner, K.U. et al. (1997) Nucleic Acids Res. 25:4323-4330). Transformed ES cells are identified and microinjected into mouse cell blastocysts such as those from the C57BL/6 mouse strain. The blastocysts are surgically transferred to pseudopregnant dams, and the resulting chimeric progeny are genotyped and bred to produce heterozygous or homozygous strains. Transgenic animals thus generated may be tested with potential therapeutic or toxic agents.

The sptm of the invention may also be manipulated in vitro in ES cells derived from human blastocysts. Human ES cells have the potential to differentiate into at least eight separate cell lineages including endoderm, mesoderm, and ectodermal cell types. These cell lineages differentiate into, for example, neural cells, hematopoietic lineages, and cardiomyocytes (Thomson, J.A. et al. (1998) Science 282:1145-1147).

The sptm of the invention can also be used to create "knockin" humanized animals (pigs) or transgenic animals (mice or rats) to model human disease. With knockin technology, a region of sptm is injected into animal ES cells, and the injected sequence integrates into the animal cell genome. Transformed cells are injected into blastulae, and the blastulae are implanted as described above. Transgenic progeny or inbred lines are studied and treated with potential pharmaceutical agents to obtain information on treatment of a human disease. Alternatively, a mammal inbred to overexpress sptm, resulting, e.g., in the secretion of SPTM in its milk, may also serve as a convenient source of that protein (Janne, J. et al. (1998) Biotechnol. Annu. Rev. 4:55-74).

Screening Assays

SPTM encoded by polynucleotides of the present invention may be used to screen for molecules that bind to or are bound by the encoded polypeptides. The binding of the polypeptide and the molecule may activate (agonist), increase, inhibit (antagonist), or decrease activity of the polypeptide or the bound molecule. Examples of such molecules include antibodies, oligonucleotides, proteins (e.g., receptors), or small molecules.

Preferably, the molecule is closely related to the natural ligand of the polypeptide, e.g., a ligand or fragment thereof, a natural substrate, or a structural or functional mimetic. (See, Coligan et al., (1991) Current Protocols in Immunology 1(2): Chapter 5.) Similarly, the molecule can be closely related to the natural receptor to which the polypeptide binds, or to at least a fragment of the receptor, e.g., the active site. In either case, the molecule can be rationally designed using known techniques. Preferably, the screening for these molecules involves producing appropriate cells which express the polypeptide, either as a secreted protein or on the cell membrane. Preferred cells include cells from mammals, yeast, Drosophila, or E. coli. Cells expressing the polypeptide or cell membrane fractions which contain the expressed polypeptide are then contacted with a test compound and binding, stimulation, or inhibition of activity of either the polypeptide or the molecule is analyzed.

An assay may simply test binding of a candidate compound to the polypeptide, wherein binding is detected by a fluorophore, radioisotope, enzyme conjugate, or other detectable label. Alternatively, the assay may assess binding in the presence of a labeled competitor.

Additionally, the assay can be carried out using cell-free preparations, polypeptide/molecule affixed to a solid support, chemical libraries, or natural product mixtures. The assay may also simply comprise the steps of mixing a candidate compound with a solution containing a polypeptide, measuring polypeptide/molecule activity or binding, and comparing the polypeptide/molecule activity or binding to a standard.

Preferably, an ELISA assay using, e.g., a monoclonal or polyclonal antibody, can measure polypeptide level in a sample. The antibody can measure polypeptide level by either binding, directly or indirectly, to the polypeptide or by competing with the polypeptide for a substrate.

All of the above assays can be used in a diagnostic or prognostic context. The molecules discovered using these assays can be used to treat disease or to bring about a particular result in a patient (e.g., blood vessel growth) by activating or inhibiting the polypeptide/molecule. Moreover, the assays can discover agents which may inhibit or enhance the production of the polypeptide from suitably manipulated cells or tissues.

Transcript Imaging

Another embodiment relates to the use of sptm to develop a transcript image of a tissue or cell type. A transcript image is the collective pattern of gene expression by a particular tissue or cell type under given conditions and at a given time. This pattern of gene expression is defined by the

number of expressed genes, their abundance, and their function. Thus the sptm of the present invention may be used to develop a transcript image of a tissue or cell type by hybridizing, preferably in a microarray format, the sptm of the present invention to the totality of transcripts or reverse transcripts of a tissue or cell type. The resultant transcript image would provide a profile of gene activity pertaining to cell signaling.

Transcript images which profile sptm expression may be generated using transcripts isolated from tissues, cell lines, biopsies, or other biological samples. The transcript image may thus reflect sptm expression in vivo, as in the case of a tissue or biopsy sample, or in vitro, as in the case of a cell line. Transcript images may be used to profile sptm expression in distinct tissue types. This process can be used to determine cell signaling activity in a particular tissue type relative to this activity in a different tissue type. Transcript images may be used to generate a profile of sptm expression characteristic of diseased tissue. Transcript images of tissues before and after treatment may be used for diagnostic purposes, to monitor the progression of disease, and to monitor the efficacy of drug treatments for diseases which affect cell signaling.

Transcript images which profile sptm expression may also be used in conjunction with in vitro model systems and preclinical evaluation of pharmaceuticals. Transcript images of cell lines can be used to assess cell signaling activity and/or to identify cell lines that lack or misregulate this activity. Such cell lines may then be treated with pharmaceutical agents, and a transcript image following treatment may indicate the efficacy of these agents in restoring desired levels of this activity. A similar approach may be used to assess the toxicity of pharmaceutical agents as reflected by undesirable changes in cell signaling. Candidate pharmaceutical agents may be evaluated by comparing their associated transcript images with those of pharmaceutical agents of known effectiveness.

Antisense Molecules

The polynucleotides of the present invention are useful in antisense technology. Antisense technology or therapy relies on the modulation of expression of a target protein through the specific binding of an antisense sequence to a target sequence encoding the target protein or directing its expression. (See, e.g., Agrawal, S., ed. (1996) Antisense Therapeutics, Humana Press Inc., Totawa NJ; Alama, A. et al. (1997) Pharmacol. Res. 36(3):171-178; Crooke, S.T. (1997) Adv. Pharmacol. 40:1-49; Sharma, H.W. and R. Narayanan (1995) Bioessays 17(12):1055-1063; and Lavrosky, Y. et al. (1997) Biochem. Mol. Med. 62(1):11-22.) An antisense sequence is a polynucleotide sequence capable of specifically hybridizing to at least a portion of the target sequence. Antisense sequences bind to cellular mRNA and/or genomic DNA, affecting translation and/or transcription. Antisense sequences can be DNA, RNA, or nucleic acid mimics and analogs. (See, e.g., Rossi, J.J. et al. (1991) Antisense Res. Dev. 1(3):285-288; Lee, R. et al. (1998) Biochemistry 37(3):900-1010; Pardridge, W.M. et al. (1995) Proc. Natl. Acad. Sci. USA 92(12):5592-5596; and Nielsen, P. E. and Haaima, G.

(1997) Chem. Soc. Rev. 96:73-78.) Typically, the binding which results in modulation of expression occurs through hybridization or binding of complementary base pairs. Antisense sequences can also bind to DNA duplexes through specific interactions in the major groove of the double helix.

The polynucleotides of the present invention and fragments thereof can be used as antisense sequences to modify the expression of the polypeptide encoded by sptm. The antisense sequences can be produced ex vivo, such as by using any of the ABI nucleic acid synthesizer series (PE Biosystems) or other automated systems known in the art. Antisense sequences can also be produced biologically, such as by transforming an appropriate host cell with an expression vector containing the sequence of interest. (See, e.g., Agrawal, supra.)

In therapeutic use, any gene delivery system suitable for introduction of the antisense sequences into appropriate target cells can be used. Antisense sequences can be delivered intracellularly in the form of an expression plasmid which, upon transcription, produces a sequence complementary to at least a portion of the cellular sequence encoding the target protein. (See, e.g., Slater, J.E., et al. (1998) J. Allergy Clin. Immunol. 102(3):469-475; and Scanlon, K.J., et al. (1995) 9(13):1288-1296.) Antisense sequences can also be introduced intracellularly through the use of viral vectors, such as retrovirus and adeno-associated virus vectors. (See, e.g., Miller, A.D. (1990) Blood 76:271; Ausubel, F.M. et al. (1995) Current Protocols in Molecular Biology, John Wiley & Sons, New York NY; Uckert, W. and W. Walther (1994) Pharmacol. Ther. 63(3):323-347.) Other gene delivery mechanisms include liposome-derived systems, artificial viral envelopes, and other systems known in the art. (See, e.g., Rossi, J.J. (1995) Br. Med. Bull. 51(1):217-225; Boado, R.J. et al. (1998) J. Pharm. Sci. 87(11):1308-1315; and Morris, M.C. et al. (1997) Nucleic Acids Res. 25(14):2730-2736.)

Expression

In order to express a biologically active SPTM, the nucleotide sequences encoding SPTM or fragments thereof may be inserted into an appropriate expression vector, i.e., a vector which contains the necessary elements for transcriptional and translational control of the inserted coding sequence in a suitable host. Methods which are well known to those skilled in the art may be used to construct expression vectors containing sequences encoding SPTM and appropriate transcriptional and translational control elements. These methods include in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. (See, e.g., Sambrook, supra, Chapters 4, 8, 16, and 17; and Ausubel, supra, Chapters 9, 10, 13, and 16.)

A variety of expression vector/host systems may be utilized to contain and express sequences encoding SPTM. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with viral expression vectors (e.g., baculovirus); plant cell systems transformed with viral expression vectors (e.g., cauliflower mosaic

virus, CaMV, or tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or animal (mammalian) cell systems. (See, e.g., Sambrook, supra; Ausubel, 1995, supra, Van Heeke, G. and S.M. Schuster (1989) J. Biol. Chem. 264:5503-5509; Bitter, G.A. et al. (1987) Methods Enzymol. 153:516-544; Scorer, C.A. et al. (1994) Bio/Technology 12:181-184; Engelhard, E.K. et al. (1994) Proc. Natl. Acad. Sci. USA 91:3224-3227; Sandig, V. et al. (1996) Hum. Gene Ther. 7:1937-1945; Takamatsu, N. (1987) EMBO J. 6:307-311; Coruzzi, G. et al. (1984) EMBO J. 3:1671-1680; Broglie, R. et al. (1984) Science 224:838-843; Winter, J. et al. (1991) Results Probl. Cell Differ. 17:85-105; The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York NY, pp. 191-196; Logan, J. and T. Shenk (1984) Proc. Natl. Acad. Sci. USA 81:3655-3659; and Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355.) Expression vectors derived from retroviruses, adenoviruses, or herpes or vaccinia viruses, or from various bacterial plasmids, may be used for delivery of nucleotide sequences to the targeted organ, tissue, or cell population. (See, e.g., Di Nicola, M. et al. (1998) Cancer Gen. Ther. 5(6):350-356; Yu, M. et al., (1993) Proc. Natl. Acad. Sci. USA 90(13):6340-6344; Buller, R.M. et al. (1985) Nature 317(6040):813-815; McGregor, D.P. et al. (1994) Mol. Immunol. 31(3):219-226; and Verma, I.M. and N. Somia (1997) Nature 389:239-242.) The invention is not limited by the host cell employed.

For long term production of recombinant proteins in mammalian systems, stable expression of SPTM in cell lines is preferred. For example, sequences encoding SPTM can be transformed into cell lines using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Any number of selection systems may be used to recover transformed cell lines. (See, e.g., Wigler, M. et al. (1977) Cell 11:223-232; Lowy, I. et al. (1980) Cell 22:817-823.; Wigler, M. et al. (1980) Proc. Natl. Acad. Sci. USA 77:3567-3570; Colbere-Garapin, F. et al. (1981) J. Mol. Biol. 150:1-14; Hartman, S.C. and R.C.Mulligan (1988) Proc. Natl. Acad. Sci. USA 85:8047-8051; Rhodes, C.A. (1995) Methods Mol. Biol. 55:121-131.)

Therapeutic Uses of sptm

The sptm of the invention may be used for somatic or germline gene therapy. Gene therapy may be performed to (i) correct a genetic deficiency (e.g., in the cases of severe combined immunodeficiency (SCID)-X1 disease characterized by X-linked inheritance (Cavazzana-Calvo, M. et al. (2000) Science 288:669-672), severe combined immunodeficiency syndrome associated with an inherited adenosine deaminase (ADA) deficiency (Blaese, R.M. et al. (1995) Science 270:475-480; Bordignon, C. et al. (1995) Science 270:470-475), cystic fibrosis (Zabner, J. et al. (1993) Cell 75:207-216; Crystal, R.G. et al. (1995) Hum. Gene Therapy 6:643-666; Crystal, R.G. et al. (1995) Hum. Gene Therapy 6:667-703), thalassemias, familial hypercholesterolemia, and hemophilia resulting from Factor VIII or Factor IX deficiencies (Crystal, R.G. (1995) Science 270:404-410; Verma, I.M. and Somia, N. (1997) Nature 389:239-242)), (ii) express a conditionally lethal gene

product (e.g., in the case of cancers which result from unregulated cell proliferation), or (iii) express a protein which affords protection against intracellular parasites (e.g., against human retroviruses, such as human immunodeficiency virus (HIV) (Baltimore, D. (1988) Nature 335:395-396; Poeschla, E. et al. (1996) Proc. Natl. Acad. Sci. USA. 93:11395-11399), hepatitis B or C virus (HBV, HCV); fungal parasites, such as Candida albicans and Paracoccidioides brasiliensis; and protozoan parasites such as Plasmodium falciparum and Trypanosoma cruzi). In the case where a genetic deficiency in sptm expression or regulation causes disease, the expression of sptm from an appropriate population of transduced cells may alleviate the clinical manifestations caused by the genetic deficiency.

In a further embodiment of the invention, diseases or disorders caused by deficiencies in sptm are treated by constructing mammalian expression vectors comprising sptm and introducing these vectors by mechanical means into sptm-deficient cells. Mechanical transfer technologies for use with cells in vivo or ex vitro include (i) direct DNA microinjection into individual cells, (ii) ballistic gold particle delivery, (iii) liposome-mediated transfection, (iv) receptor-mediated gene transfer, and (v) the use of DNA transposons (Morgan, R.A. and Anderson, W.F. (1993) Annu. Rev. Biochem. 62:191-217; Ivics, Z. (1997) Cell 91:501-510; Boulay, J-L. and Récipon, H. (1998) Curr. Opin. Biotechnol. 9:445-450).

Expression vectors that may be effective for the expression of sptm include, but are not limited to, the PCDNA 3.1, EPITAG, PRCCMV2, PREP, PVAX vectors (Invitrogen, Carlsbad CA), PCMV-SCRIPT, PCMV-TAG, PEGSH/PERV (Stratagene, La Jolla CA), and PTET-OFF, PTET-ON, PTRE2, PTRE2-LUC, PTK-HYG (Clontech, Palo Alto CA). The sptm of the invention may be expressed using (i) a constitutively active promoter, (e.g., from cytomegalovirus (CMV), Rous sarcoma virus (RSV), SV40 virus, thymidine kinase (TK), or β-actin genes), (ii) an inducible promoter (e.g., the tetracycline-regulated promoter (Gossen, M. and Bujard, H. (1992) Proc. Natl. Acad. Sci. U.S.A. 89:5547-5551; Gossen, M. et al., (1995) Science 268:1766-1769; Rossi, F.M.V. and Blau, H.M. (1998) Curr. Opin. Biotechnol. 9:451-456), commercially available in the T-REX plasmid (Invitrogen)); the ecdysone-inducible promoter (available in the plasmids PVGRXR and PIND; Invitrogen); the FK506/rapamycin inducible promoter; or the RU486/mifepristone inducible promoter (Rossi, F.M.V. and Blau, H.M. supra)), or (iii) a tissue-specific promoter or the native promoter of the endogenous gene encoding SPTM from a normal individual.

Commercially available liposome transformation kits (e.g., the PERFECT LIPID TRANSFECTION KIT, available from Invitrogen) allow one with ordinary skill in the art to deliver polynucleotides to target cells in culture and require minimal effort to optimize experimental parameters. In the alternative, transformation is performed using the calcium phosphate method (Graham, F.L. and Eb, A.J. (1973) Virology 52:456-467), or by electroporation (Neumann, E. et al. (1982) EMBO J. 1:841-845). The introduction of DNA to primary cells requires modification of these standardized mammalian transfection protocols.

In another embodiment of the invention, diseases or disorders caused by genetic defects with respect to sptm expression are treated by constructing a retrovirus vector consisting of (i) sptm under the control of an independent promoter or the retrovirus long terminal repeat (LTR) promoter, (ii) appropriate RNA packaging signals, and (iii) a Rev-responsive element (RRE) along with additional retrovirus *cis*-acting RNA sequences and coding sequences required for efficient vector propagation. Retrovirus vectors (e.g., PFB and PFBNEO) are commercially available (Stratagene) and are based on published data (Riviere, I. et al. (1995) Proc. Natl. Acad. Sci. U.S.A. 92:6733-6737), incorporated by reference herein. The vector is propagated in an appropriate vector producing cell line (VPCL) that expresses an envelope gene with a tropism for receptors on the target cells or a promiscuous envelope protein such as VSVg (Armentano, D. et al. (1987) J. Virol. 61:1647-1650; Bender, M.A. et al. (1987) J. Virol. 61:1639-1646; Adam, M.A. and Miller, A.D. (1988) J. Virol. 62:3802-3806; Dull, T. et al. (1998) J. Virol. 72:8463-8471; Zufferey, R. et al. (1998) J. Virol. 72:9873-9880). U.S. Patent Number 5,910,434 to Rigg ("Method for obtaining retrovirus packaging cell lines producing high transducing efficiency retroviral supernatant") discloses a method for obtaining retrovirus packaging cell lines and is hereby incorporated by reference. Propagation of retrovirus vectors, transduction of a population of cells (e.g., $CD4^+$ T-cells), and the return of transduced cells to a patient are procedures well known to persons skilled in the art of gene therapy and have been well documented (Ranga, U. et al. (1997) J. Virol. 71:7020-7029; Bauer, G. et al. (1997) Blood 89:2259-2267; Bonyhadi, M.L. (1997) J. Virol. 71:4707-4716; Ranga, U. et al. (1998) Proc. Natl. Acad. Sci. U.S.A. 95:1201-1206; Su, L. (1997) Blood 89:2283-2290).

In the alternative, an adenovirus-based gene therapy delivery system is used to deliver sptm to cells which have one or more genetic abnormalities with respect to the expression of sptm. The construction and packaging of adenovirus-based vectors are well known to those with ordinary skill in the art. Replication defective adenovirus vectors have proven to be versatile for importing genes encoding immunoregulatory proteins into intact islets in the pancreas (Csete, M.E. et al. (1995) Transplantation 27:263-268). Potentially useful adenoviral vectors are described in U.S. Patent Number 5,707,618 to Armentano ("Adenovirus vectors for gene therapy"), hereby incorporated by reference. For adenoviral vectors, see also Antinozzi, P.A. et al. (1999) Annu. Rev. Nutr. 19:511-544 and Verma, I.M. and Somia, N. (1997) Nature 18:389:239-242, both incorporated by reference herein.

In another alternative, a herpes-based, gene therapy delivery system is used to deliver sptm to target cells which have one or more genetic abnormalities with respect to the expression of sptm. The use of herpes simplex virus (HSV)-based vectors may be especially valuable for introducing sptm to cells of the central nervous system, for which HSV has a tropism. The construction and packaging of herpes-based vectors are well known to those with ordinary skill in the art. A replication-competent herpes simplex virus (HSV) type 1-based vector has been used to deliver a

reporter gene to the eyes of primates (Liu, X. et al. (1999) Exp. Eye Res.169:385-395). The construction of a HSV-1 virus vector has also been disclosed in detail in U.S. Patent Number 5,804,413 to DeLuca ("Herpes simplex virus strains for gene transfer"), which is hereby incorporated by reference. U.S. Patent Number 5,804,413 teaches the use of recombinant HSV d92 which consists of a genome containing at least one exogenous gene to be transferred to a cell under the control of the appropriate promoter for purposes including human gene therapy. Also taught by this patent are the construction and use of recombinant HSV strains deleted for ICP4, ICP27 and ICP22. For HSV vectors, see also Goins, W. F. et al. 1999 J. Virol. 73:519-532 and Xu, H. et al., (1994) Dev. Biol. 163:152-161, hereby incorporated by reference. The manipulation of cloned herpesvirus sequences, the generation of recombinant virus following the transfection of multiple plasmids containing different segments of the large herpesvirus genomes, the growth and propagation of herpesvirus, and the infection of cells with herpesvirus are techniques well known to those of ordinary skill in the art.

In another alternative, an alphavirus (positive, single-stranded RNA virus) vector is used to deliver sptm to target cells. The biology of the prototypic alphavirus, Semliki Forest Virus (SFV), has been studied extensively and gene transfer vectors have been based on the SFV genome (Garoff, H. and Li, K-J. (1998) Curr. Opin. Biotech. 9:464-469). During alphavirus RNA replication, a subgenomic RNA is generated that normally encodes the viral capsid proteins. This subgenomic RNA replicates to higher levels than the full-length genomic RNA, resulting in the overproduction of capsid proteins relative to the viral proteins with enzymatic activity (e.g., protease and polymerase). Similarly, inserting sptm into the alphavirus genome in place of the capsid-coding region results in the production of a large number of sptm RNAs and the synthesis of high levels of SPTM in vector transduced cells. While alphavirus infection is typically associated with cell lysis within a few days, the ability to establish a persistent infection in hamster normal kidney cells (BHK-21) with a variant of Sindbis virus (SIN) indicates that the lytic replication of alphaviruses can be altered to suit the needs of the gene therapy application (Dryga, S.A. et al. (1997) Virology 228:74-83). The wide host range of alphaviruses will allow the introduction of SPTM into a variety of cell types. The specific transduction of a subset of cells in a population may require the sorting of cells prior to transduction. The methods of manipulating infectious cDNA clones of alphaviruses, performing alphavirus cDNA and RNA transfections, and performing alphavirus infections, are well known to those with ordinary skill in the art.

Antibodies

Anti-SPTM antibodies may be used to analyze protein expression levels. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, and Fab fragments.

For descriptions of and protocols of antibody technologies, see, e.g., Pound J.D. (1998) Immunochemical Protocols, Humana Press, Totowa, NJ.

The amino acid sequence encoded by the sptm of the Sequence Listing may be analyzed by appropriate software (e.g., LASERGENE NAVIGATOR software, DNASTAR) to determine regions of high immunogenicity. The optimal sequences for immunization are selected from the C-terminus, the N-terminus, and those intervening, hydrophilic regions of the polypeptide which are likely to be exposed to the external environment when the polypeptide is in its natural conformation. Analysis used to select appropriate epitopes is also described by Ausubel (1997, supra, Chapter 11.7). Peptides used for antibody induction do not need to have biological activity; however, they must be antigenic. Peptides used to induce specific antibodies may have an amino acid sequence consisting of at five amino acids, preferably at least 10 amino acids, and most preferably 15 amino acids. A peptide which mimics an antigenic fragment of the natural polypeptide may be fused with another protein such as keyhole limpet cyanin (KLH; Sigma, St. Louis MO) for antibody production. A peptide encompassing an antigenic region may be expressed from an sptm, synthesized as described above, or purified from human cells.

Procedures well known in the art may be used for the production of antibodies. Various hosts including mice, goats, and rabbits, may be immunized by injection with a peptide. Depending on the host species, various adjuvants may be used to increase immunological response.

In one procedure, peptides about 15 residues in length may be synthesized using an ABI 431A peptide synthesizer (PE Biosystems) using fmoc-chemistry and coupled to KLH (Sigma) by reaction with M-maleimidobenzoyl-N-hydroxysuccinimide ester (Ausubel, 1995, supra). Rabbits are immunized with the peptide-KLH complex in complete Freund's adjuvant. The resulting antisera are tested for antipeptide activity by binding the peptide to plastic, blocking with 1% bovine serum albumin (BSA), reacting with rabbit antisera, washing, and reacting with radioiodinated goat anti-rabbit IgG. Antisera with antipeptide activity are tested for anti-SPTM activity using protocols well known in the art, including ELISA, radioimmunoassay (RIA), and immunoblotting.

In another procedure, isolated and purified peptide may be used to immunize mice (about 100 μg of peptide) or rabbits (about 1 mg of peptide). Subsequently, the peptide is radioiodinated and used to screen the immunized animals' B-lymphocytes for production of antipeptide antibodies. Positive cells are then used to produce hybridomas using standard techniques. About 20 mg of peptide is sufficient for labeling and screening several thousand clones. Hybridomas of interest are detected by screening with radioiodinated peptide to identify those fusions producing peptide-specific monoclonal antibody. In a typical protocol, wells of a multi-well plate (FAST, Becton-Dickinson, Palo Alto, CA) are coated with affinity-purified, specific rabbit-anti-mouse (or suitable anti-species IgG) antibodies at 10 mg/ml. The coated wells are blocked with 1% BSA and washed

and exposed to supernatants from hybridomas. After incubation, the wells are exposed to radiolabeled peptide at 1 mg/ml.

Clones producing antibodies bind a quantity of labeled peptide that is detectable above background. Such clones are expanded and subjected to 2 cycles of cloning. Cloned hybridomas are injected into pristane-treated mice to produce ascites, and monoclonal antibody is purified from the ascitic fluid by affinity chromatography on protein A (Amersham Pharmacia Biotech). Several procedures for the production of monoclonal antibodies, including in vitro production, are described in Pound (supra). Monoclonal antibodies with antipeptide activity are tested for anti-SPTM activity using protocols well known in the art, including ELISA, RIA, and immunoblotting.

Antibody fragments containing specific binding sites for an epitope may also be generated. For example, such fragments include, but are not limited to, the F(ab')2 fragments produced by pepsin digestion of the antibody molecule, and the Fab fragments generated by reducing the disulfide bridges of the F(ab')2 fragments. Alternatively, construction of Fab expression libraries in filamentous bacteriophage allows rapid and easy identification of monoclonal fragments with desired specificity (Pound, supra, Chaps. 45-47). Antibodies generated against polypeptide encoded by sptm can be used to purify and characterize full-length SPTM protein and its activity, binding partners, etc.

Assays Using Antibodies

Anti-SPTM antibodies may be used in assays to quantify the amount of SPTM found in a particular human cell. Such assays include methods utilizing the antibody and a label to detect expression level under normal or disease conditions. The peptides and antibodies of the invention may be used with or without modification or labeled by joining them, either covalently or noncovalently, with a reporter molecule.

Protocols for detecting and measuring protein expression using either polyclonal or monoclonal antibodies are well known in the art. Examples include ELISA, RIA, and fluorescent activated cell sorting (FACS). Such immunoassays typically involve the formation of complexes between the SPTM and its specific antibody and the measurement of such complexes. These and other assays are described in Pound (supra).

Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The following preferred specific embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

The disclosures of all patents, applications, and publications mentioned above and below, in particular U.S. Ser. No. 60/147,501, and U.S. Ser. No. 60/147,500 are hereby expressly incorporated by reference.

EXAMPLES

I. Construction of cDNA Libraries

RNA was purchased from CLONTECH Laboratories, Inc. (Palo Alto CA) or isolated from various tissues. Some tissues were homogenized and lysed in guanidinium isothiocyanate, while others were homogenized and lysed in phenol or in a suitable mixture of denaturants, such as TRIZOL (Life Technologies), a monophasic solution of phenol and guanidine isothiocyanate. The resulting lysates were centrifuged over CsCl cushions or extracted with chloroform. RNA was precipitated with either isopropanol or sodium acetate and ethanol, or by other routine methods.

Phenol extraction and precipitation of RNA were repeated as necessary to increase RNA purity. In most cases, RNA was treated with DNase. For most libraries, poly(A+) RNA was isolated using oligo d(T)-coupled paramagnetic particles (Promega Corporation (Promega), Madison WI), OLIGOTEX latex particles (QIAGEN, Inc. (QIAGEN), Valencia CA), or an OLIGOTEX mRNA purification kit (QIAGEN). Alternatively, RNA was isolated directly from tissue lysates using other RNA isolation kits, e.g., the POLY(A)PURE mRNA purification kit (Ambion, Inc., Austin TX).

In some cases, Stratagene was provided with RNA and constructed the corresponding cDNA libraries. Otherwise, cDNA was synthesized and cDNA libraries were constructed with the UNIZAP vector system (Stratagene Cloning Systems, Inc. (Stratagene), La Jolla CA) or SUPERSCRIPT plasmid system (Life Technologies), using the recommended procedures or similar methods known in the art. (See, e.g., Ausubel, 1997, supra, Chapters 5.1 through 6.6.) Reverse transcription was initiated using oligo d(T) or random primers. Synthetic oligonucleotide adapters were ligated to double stranded cDNA, and the cDNA was digested with the appropriate restriction enzyme or enzymes. For most libraries, the cDNA was size-selected (300-1000 bp) using SEPHACRYL S1000, SEPHAROSE CL2B, or SEPHAROSE CL4B column chromatography (Amersham Pharmacia Biotech) or preparative agarose gel electrophoresis. cDNAs were ligated into compatible restriction enzyme sites of the polylinker of a suitable plasmid, e.g., PBLUESCRIPT plasmid (Stratagene), pSPORT1 plasmid (Life Technologies), or pINCY (Incyte). Recombinant plasmids were transformed into competent E. coli cells including XL1-Blue, XL1-BlueMRF, or SOLR from Stratagene or DH5α, DH10B, or ElectroMAX DH10B from Life Technologies.

II. Isolation of cDNA Clones

Plasmids were recovered from host cells by in vivo excision using the UNIZAP vector system (Stratagene) or by cell lysis. Plasmids were purified using at least one of the following: the Magic or WIZARD Minipreps DNA purification system (Promega); the AGTC Miniprep purification kit (Edge BioSystems, Gaithersburg MD); and the QIAWELL 8, QIAWELL 8 Plus, and QIAWELL 8 Ultra plasmid purification systems or the R.E.A.L. PREP 96 plasmid purification kit

(QIAGEN). Following precipitation, plasmids were resuspended in 0.1 ml of distilled water and stored, with or without lyophilization, at 4°C.

Alternatively, plasmid DNA was amplified from host cell lysates using direct link PCR in a high-throughput format. (Rao, V.B. (1994) Anal. Biochem. 216:1-14.) Host cell lysis and thermal cycling steps were carried out in a single reaction mixture. Samples were processed and stored in 384-well plates, and the concentration of amplified plasmid DNA was quantified fluorometrically using PICOGREEN dye (Molecular Probes, Inc. (Molecular Probes), Eugene OR) and a FLUOROSKAN II fluorescence scanner (Labsystems Oy, Helsinki, Finland).

III. Sequencing and Analysis

cDNA sequencing reactions were processed using standard methods or high-throughput instrumentation such as the ABI CATALYST 800 thermal cycler (PE Biosystems) or the PTC-200 thermal cycler (MJ Research) in conjunction with the HYDRA microdispenser (Robbins Scientific Corp., Sunnyvale CA) or the MICROLAB 2200 liquid transfer system (Hamilton). cDNA sequencing reactions were prepared using reagents provided by Amersham Pharmacia Biotech or supplied in ABI sequencing kits such as the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (PE Biosystems). Electrophoretic separation of cDNA sequencing reactions and detection of labeled polynucleotides were carried out using the MEGABACE 1000 DNA sequencing system (Molecular Dynamics); the ABI PRISM 373 or 377 sequencing system (PE Biosystems) in conjunction with standard ABI protocols and base calling software; or other sequence analysis systems known in the art. Reading frames within the cDNA sequences were identified using standard methods (reviewed in Ausubel, 1997, supra, Chapter 7.7). Some of the cDNA sequences were selected for extension using the techniques disclosed in Example VIII.

IV. Assembly and Analysis of Sequences

Component sequences from chromatograms were subject to PHRED analysis and assigned a quality score. The sequences having at least a required quality score were subject to various pre-processing editing pathways to eliminate, e.g., low quality 3' ends, vector and linker sequences, polyA tails, Alu repeats, mitochondrial and ribosomal sequences, bacterial contamination sequences, and sequences smaller than 50 base pairs. In particular, low-information sequences and repetitive elements (e.g., dinucleotide repeats, Alu repeats, etc.) were replaced by "n's", or masked, to prevent spurious matches.

Processed sequences were then subject to assembly procedures in which the sequences were assigned to gene bins (bins). Each sequence could only belong to one bin. Sequences in each gene bin were assembled to produce consensus sequences (templates). Subsequent new sequences were added to existing bins using BLASTn (v.1.4 WashU) and CROSSMATCH. Candidate pairs were

identified as all BLAST hits having a quality score greater than or equal to 150. Alignments of at least 82% local identity were accepted into the bin. The component sequences from each bin were assembled using a version of PHRAP. Bins with several overlapping component sequences were assembled using DEEP PHRAP. The orientation (sense or antisense) of each assembled template was determined based on the number and orientation of its component sequences. Template sequences as disclosed in the sequence listing correspond to sense strand sequences (the "forward" reading frames), to the best determination. The complementary (antisense) strands are inherently disclosed herein. The component sequences which were used to assemble each template consensus sequence are listed in Table 3, along with their positions along the template nucleotide sequences.

Bins were compared against each other and those having local similarity of at least 82% were combined and reassembled. Reassembled bins having templates of insufficient overlap (less than 95% local identity) were re-split. Assembled templates were also subject to analysis by STITCHER/EXON MAPPER algorithms which analyze the probabilities of the presence of splice variants, alternatively spliced exons, splice junctions, differential expression of alternative spliced genes across tissue types or disease states, etc. These resulting bins were subject to several rounds of the above assembly procedures.

Once gene bins were generated based upon sequence alignments, bins were clone joined based upon clone information. If the 5' sequence of one clone was present in one bin and the 3' sequence from the same clone was present in a different bin, it was likely that the two bins actually belonged together in a single bin. The resulting combined bins underwent assembly procedures to regenerate the consensus sequences.

The final assembled templates were subsequently annotated using the following procedure. Template sequences were analyzed using BLASTn (v2.0, NCBI) versus gbpri (GenBank version 116). "Hits" were defined as an exact match having from 95% local identity over 200 base pairs through 100% local identity over 100 base pairs, or a homolog match having an E-value, i.e. a probability score, of $\leq 1 \times 10^{-8}$. The hits were subject to frameshift FASTx versus GENPEPT (GenBank version 116). (See Table 4). In this analysis, a homolog match was defined as having an E-value of $\leq 1 \times 10^{-8}$. The assembly method used above was described in "System and Methods for Analyzing Biomolecular Sequences," U.S.S.N. 09/276,534, filed March 25, 1999, and the LIFESEQ Gold user manual (Incyte) both incorporated by reference herein.

Following assembly, template sequences were subjected to motif, BLAST, and functional analyses, and categorized in protein hierarchies using methods described in, e.g., "Database System Employing Protein Function Hierarchies for Viewing Biomolecular Sequence Data," U.S.S.N. 08/812,290, filed March 6, 1997; "Relational Database for Storing Biomolecule Information," U.S.S.N. 08/947,845, filed October 9, 1997; "Project-Based Full-Length Biomolecular Sequence Database," U.S.S.N. 08/811,758, filed March 6, 1997; and "Relational Database and System for

Storing Information Relating to Biomolecular Sequences," U.S.S.N. 09/034,807, filed March 4, 1998, all of which are incorporated by reference herein.

The template sequences are further analyzed by translating each template in all three forward reading frames and searching each translation against the Pfam database of hidden Markov model-based protein families and domains using the HMMER software package (available to the public from Washington University School of Medicine, St. Louis MO). (See also World Wide Web site http://pfam.wustl.edu/ for detailed descriptions of Pfam protein domains and families.)

Additionally, the template sequences were translated in all three forward reading frames and each translation was searched against hidden Markov models for signal peptide and transmembrane domains using the HMMER software package. Construction of hidden Markov models and their usage in sequence analysis has been described. (See, for example, Eddy, S.R. (1996) Curr. Opin. Str. Biol. 6:361-365.) Segments of templates which, when translated, contain similarity to signal peptide or transmembrane domain consensus sequences are reported in Table 2. Only those signal peptide or transmembrane hits with a cutoff score of 11 bits or greater are reported. A cutoff score of 11 bits or greater corresponds to at least about 91-94% true-positives in signal peptide prediction, and at least about 75% true-positives in transmembrane domain prediction.

The results of BLAST analysis as reported in Table 1 may support the results of HMMER analysis as reported in Table 2 or may suggest alternative or additional properties of template-encoded secretory polypeptides not previously uncovered by HMMER or other analyses.

Template sequences are further analyzed using the bioinformatics tools listed in Table 4, or using sequence analysis software known in the art such as MACDNASIS PRO software (Hitachi Software Engineering, South San Francisco CA) and LASERGENE software (DNASTAR). Template sequences may be further queried against public databases such as the GenBank rodent, mammalian, vertebrate, prokaryote, and eukaryote databases.

V. Analysis of Polynucleotide Expression

Northern analysis is a laboratory technique used to detect the presence of a transcript of a gene and involves the hybridization of a labeled nucleotide sequence to a membrane on which RNAs from a particular cell type or tissue have been bound. (See, e.g., Sambrook, supra, ch. 7; Ausubel, 1995, supra, ch. 4 and 16.)

Analogous computer techniques applying BLAST are used to search for identical or related molecules in cDNA databases such as GenBank or LIFESEQ (Incyte Pharmaceuticals). This analysis is much faster than multiple membrane-based hybridizations. In addition, the sensitivity of the computer search can be modified to determine whether any particular match is categorized as exact or similar. The basis of the search is the product score, which is defined as:

$$\frac{\text{BLAST Score x Percent Identity}}{\text{5 x minimum \{length(Seq. 1), length(Seq. 2)\}}}$$

The product score takes into account both the degree of similarity between two sequences and the length of the sequence match. The product score is a normalized value between 0 and 100, and is calculated as follows: the BLAST score is multiplied by the percent nucleotide identity and the product is divided by (5 times the length of the shorter of the two sequences). The BLAST score is calculated by assigning a score of +5 for every base that matches in a high-scoring segment pair (HSP), and -4 for every mismatch. Two sequences may share more than one HSP (separated by gaps). If there is more than one HSP, then the pair with the highest BLAST score is used to calculate the product score. The product score represents a balance between fractional overlap and quality in a BLAST alignment. For example, a product score of 100 is produced only for 100% identity over the entire length of the shorter of the two sequences being compared. A product score of 70 is produced either by 100% identity and 70% overlap at one end, or by 88% identity and 100% overlap at the other. A product score of 50 is produced either by 100% identity and 50% overlap at one end, or 79% identity and 100% overlap.

VI. Tissue Distribution Profiling

A tissue distribution profile is determined for each template by compiling the cDNA library tissue classifications of its component cDNA sequences. Each component sequence, is derived from a cDNA library constructed from a human tissue. Each human tissue is classified into one of the following categories: cardiovascular system; connective tissue; digestive system; embryonic structures; endocrine system; exocrine glands; genitalia, female; genitalia, male; germ cells; hemic and immune system; liver; musculoskeletal system; nervous system; pancreas; respiratory system; sense organs; skin; stomatognathic system; unclassified/mixed; or urinary tract. Template sequences, component sequences, and cDNA library/tissue information are found in the LIFESEQ GOLD database (Incyte Genomics, Palo Alto CA).

VII. Transcript Image Analysis

Transcript images are generated as described in Seilhamer et al., "Comparative Gene Transcript Analysis," U.S. Patent Number 5,840,484, incorporated herein by reference.

VIII. Extension of Polynucleotide Sequences and Isolation of a Full-length cDNA

Oligonucleotide primers designed using an sptm of the Sequence Listing are used to extend the nucleic acid sequence. One primer is synthesized to initiate 5' extension of the template, and the other primer, to initiate 3' extension of the template. The initial primers may be designed using

OLIGO 4.06 software (National Biosciences, Inc. (National Biosciences), Plymouth MN), or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the target sequence at temperatures of about 68°C to about 72°C. Any stretch of nucleotides which would result in hairpin structures and primer-primer dimerizations are avoided. Selected human cDNA libraries are used to extend the sequence. If more than one extension is necessary or desired, additional or nested sets of primers are designed.

High fidelity amplification is obtained by PCR using methods well known in the art. PCR is performed in 96-well plates using the PTC-200 thermal cycler (MJ Research). The reaction mix contains DNA template, 200 nmol of each primer, reaction buffer containing Mg^{2+}, $(NH_4)_2SO_4$, and ß-mercaptoethanol, Taq DNA polymerase (Amersham Pharmacia Biotech), ELONGASE enzyme (Life Technologies), and Pfu DNA polymerase (Stratagene), with the following parameters for primer pair PCI A and PCI B: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C. In the alternative, the parameters for primer pair T7 and SK+ are as follows: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 57°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C.

The concentration of DNA in each well is determined by dispensing 100 µl PICOGREEN quantitation reagent (0.25% (v/v); Molecular Probes) dissolved in 1X Tris-EDTA (TE) and 0.5 µl of undiluted PCR product into each well of an opaque fluorimeter plate (Corning Incorporated (Corning), Corning NY), allowing the DNA to bind to the reagent. The plate is scanned in a FLUOROSKAN II (Labsystems Oy) to measure the fluorescence of the sample and to quantify the concentration of DNA. A 5 µl to 10 µl aliquot of the reaction mixture is analyzed by electrophoresis on a 1 % agarose mini-gel to determine which reactions are successful in extending the sequence.

The extended nucleotides are desalted and concentrated, transferred to 384-well plates, digested with CviJI cholera virus endonuclease (Molecular Biology Research, Madison WI), and sonicated or sheared prior to religation into pUC 18 vector (Amersham Pharmacia Biotech). For shotgun sequencing, the digested nucleotides are separated on low concentration (0.6 to 0.8%) agarose gels, fragments are excised, and agar digested with AGAR ACE (Promega). Extended clones are religated using T4 ligase (New England Biolabs, Inc., Beverly MA) into pUC 18 vector (Amersham Pharmacia Biotech), treated with Pfu DNA polymerase (Stratagene) to fill-in restriction site overhangs, and transfected into competent E. coli cells. Transformed cells are selected on antibiotic-containing media, individual colonies are picked and cultured overnight at 37°C in 384-well plates in LB/2x carbenicillin liquid media.

The cells are lysed, and DNA is amplified by PCR using Taq DNA polymerase (Amersham Pharmacia Biotech) and Pfu DNA polymerase (Stratagene) with the following parameters: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 72°C, 2 min; Step 5: steps 2, 3, and

4 repeated 29 times; Step 6: 72°C, 5 min; Step 7: storage at 4°C. DNA is quantified by PICOGREEN reagent (Molecular Probes) as described above. Samples with low DNA recoveries are reamplified using the same conditions as described above. Samples are diluted with 20% dimethysulfoxide (1:2, v/v), and sequenced using DYENAMIC energy transfer sequencing primers and the DYENAMIC DIRECT kit (Amersham Pharmacia Biotech) or the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (PE Biosystems).

In like manner, the sptm is used to obtain regulatory sequences (promoters, introns, and enhancers) using the procedure above, oligonucleotides designed for such extension, and an appropriate genomic library.

IX. Labeling of Probes and Southern Hybridization Analyses

Hybridization probes derived from the sptm of the Sequence Listing are employed for screening cDNAs, mRNAs, or genomic DNA. The labeling of probe nucleotides between 100 and 1000 nucleotides in length is specifically described, but essentially the same procedure may be used with larger cDNA fragments. Probe sequences are labeled at room temperature for 30 minutes using a T4 polynucleotide kinase, γ^{32}P-ATP, and 0.5X One-Phor-All Plus (Amersham Pharmacia Biotech) buffer and purified using a ProbeQuant G-50 Microcolumn (Amersham Pharmacia Biotech). The probe mixture is diluted to 10^7 dpm/µg/ml hybridization buffer and used in a typical membrane-based hybridization analysis.

The DNA is digested with a restriction endonuclease such as Eco RV and is electrophoresed through a 0.7% agarose gel. The DNA fragments are transferred from the agarose to nylon membrane (NYTRAN Plus, Schleicher & Schuell, Inc., Keene NH) using procedures specified by the manufacturer of the membrane. Prehybridization is carried out for three or more hours at 68°C, and hybridization is carried out overnight at 68°C. To remove non-specific signals, blots are sequentially washed at room temperature under increasingly stringent conditions, up to 0.1x saline sodium citrate (SSC) and 0.5% sodium dodecyl sulfate. After the blots are placed in a PHOSPHORIMAGER cassette (Molecular Dynamics) or are exposed to autoradiography film, hybridization patterns of standard and experimental lanes are compared. Essentially the same procedure is employed when screening RNA.

X. Chromosome Mapping of sptm

The cDNA sequences which were used to assemble SEQ ID NO:1-26 are compared with sequences from the Incyte LIFESEQ database and public domain databases using BLAST and other implementations of the Smith-Waterman algorithm. Sequences from these databases that match SEQ ID NO:1-26 are assembled into clusters of contiguous and overlapping sequences using assembly algorithms such as PHRAP (Table 4). Radiation hybrid and genetic mapping data available from

public resources such as the Stanford Human Genome Center (SHGC), Whitehead Institute for Genome Research (WIGR), and Généthon are used to determine if any of the clustered sequences have been previously mapped. Inclusion of a mapped sequence in a cluster will result in the assignment of all sequences of that cluster, including its particular SEQ ID NO:, to that map location. The genetic map locations of SEQ ID NO:1-26 are described as ranges, or intervals, of human chromosomes. The map position of an interval, in centiMorgans, is measured relative to the terminus of the chromosome's p-arm. (The centiMorgan (cM) is a unit of measurement based on recombination frequencies between chromosomal markers. On average, 1 cM is roughly equivalent to 1 megabase (Mb) of DNA in humans, although this can vary widely due to hot and cold spots of recombination.) The cM distances are based on genetic markers mapped by Généthon which provide boundaries for radiation hybrid markers whose sequences were included in each of the clusters.

XI. Microarray Analysis

Probe Preparation from Tissue or Cell Samples

Total RNA is isolated from tissue samples using the guanidinium thiocyanate method and polyA$^+$ RNA is purified using the oligo (dT) cellulose method. Each polyA$^+$ RNA sample is reverse transcribed using MMLV reverse-transcriptase, 0.05 pg/µl oligo-dT primer (21mer), 1X first strand buffer, 0.03 units/µl RNase inhibitor, 500 µM dATP, 500 µM dGTP, 500 µM dTTP, 40 µM dCTP, 40 µM dCTP-Cy3 (BDS) or dCTP-Cy5 (Amersham Pharmacia Biotech). The reverse transcription reaction is performed in a 25 ml volume containing 200 ng polyA$^+$ RNA with GEMBRIGHT kits (Incyte). Specific control polyA$^+$ RNAs are synthesized by in vitro transcription from non-coding yeast genomic DNA (W. Lei, unpublished). As quantitative controls, the control mRNAs at 0.002 ng, 0.02 ng, 0.2 ng, and 2 ng are diluted into reverse transcription reaction at ratios of 1:100,000, 1:10,000, 1:1000, 1:100 (w/w) to sample mRNA respectively. The control mRNAs are diluted into reverse transcription reaction at ratios of 1:3, 3:1, 1:10, 10:1, 1:25, 25:1 (w/w) to sample mRNA differential expression patterns. After incubation at 37°C for 2 hr, each reaction sample (one with Cy3 and another with Cy5 labeling) is treated with 2.5 ml of 0.5M sodium hydroxide and incubated for 20 minutes at 85°C to the stop the reaction and degrade the RNA. Probes are purified using two successive CHROMA SPIN 30 gel filtration spin columns (CLONTECH Laboratories, Inc. (CLONTECH), Palo Alto CA) and after combining, both reaction samples are ethanol precipitated using 1 ml of glycogen (1 mg/ml), 60 ml sodium acetate, and 300 ml of 100% ethanol. The probe is then dried to completion using a SpeedVAC (Savant Instruments Inc., Holbrook NY) and resuspended in 14 µl 5X SSC/0.2% SDS.

Microarray Preparation

Sequences of the present invention are used to generate array elements. Each array element is amplified from bacterial cells containing vectors with cloned cDNA inserts. PCR amplification

uses primers complementary to the vector sequences flanking the cDNA insert. Array elements are amplified in thirty cycles of PCR from an initial quantity of 1-2 ng to a final quantity greater than 5 μg. Amplified array elements are then purified using SEPHACRYL-400 (Amersham Pharmacia Biotech).

Purified array elements are immobilized on polymer-coated glass slides. Glass microscope slides (Corning) are cleaned by ultrasound in 0.1% SDS and acetone, with extensive distilled water washes between and after treatments. Glass slides are etched in 4% hydrofluoric acid (VWR Scientific Products Corporation (VWR), West Chester, PA), washed extensively in distilled water, and coated with 0.05% aminopropyl silane (Sigma) in 95% ethanol. Coated slides are cured in a 110°C oven.

Array elements are applied to the coated glass substrate using a procedure described in US Patent No. 5,807,522, incorporated herein by reference. 1 μl of the array element DNA, at an average concentration of 100 ng/μl, is loaded into the open capillary printing element by a high-speed robotic apparatus. The apparatus then deposits about 5 nl of array element sample per slide.

Microarrays are UV-crosslinked using a STRATALINKER UV-crosslinker (Stratagene). Microarrays are washed at room temperature once in 0.2% SDS and three times in distilled water. Non-specific binding sites are blocked by incubation of microarrays in 0.2% casein in phosphate buffered saline (PBS) (Tropix, Inc., Bedford, MA) for 30 minutes at 60°C followed by washes in 0.2% SDS and distilled water as before.

Hybridization

Hybridization reactions contain 9 μl of probe mixture consisting of 0.2 μg each of Cy3 and Cy5 labeled cDNA synthesis products in 5X SSC, 0.2% SDS hybridization buffer. The probe mixture is heated to 65°C for 5 minutes and is aliquoted onto the microarray surface and covered with an 1.8 cm^2 coverslip. The arrays are transferred to a waterproof chamber having a cavity just slightly larger than a microscope slide. The chamber is kept at 100% humidity internally by the addition of 140 μl of 5x SSC in a corner of the chamber. The chamber containing the arrays is incubated for about 6.5 hours at 60°C. The arrays are washed for 10 min at 45°C in a first wash buffer (1X SSC, 0.1% SDS), three times for 10 minutes each at 45°C in a second wash buffer (0.1X SSC), and dried.

Detection

Reporter-labeled hybridization complexes are detected with a microscope equipped with an Innova 70 mixed gas 10 W laser (Coherent, Inc., Santa Clara CA) capable of generating spectral lines at 488 nm for excitation of Cy3 and at 632 nm for excitation of Cy5. The excitation laser light is focused on the array using a 20X microscope objective (Nikon, Inc., Melville NY). The slide containing the array is placed on a computer-controlled X-Y stage on the microscope and raster-

scanned past the objective. The 1.8 cm x 1.8 cm array used in the present example is scanned with a resolution of 20 micrometers..

In two separate scans, a mixed gas multiline laser excites the two fluorophores sequentially. Emitted light is split, based on wavelength, into two photomultiplier tube detectors (PMT R1477, Hamamatsu Photonics Systems, Bridgewater NJ) corresponding to the two fluorophores. Appropriate filters positioned between the array and the photomultiplier tubes are used to filter the signals. The emission maxima of the fluorophores used are 565 nm for Cy3 and 650 nm for Cy5. Each array is typically scanned twice, one scan per fluorophore using the appropriate filters at the laser source, although the apparatus is capable of recording the spectra from both fluorophores simultaneously.

The sensitivity of the scans is typically calibrated using the signal intensity generated by a cDNA control species added to the probe mix at a known concentration. A specific location on the array contains a complementary DNA sequence, allowing the intensity of the signal at that location to be correlated with a weight ratio of hybridizing species of 1:100,000. When two probes from different sources (e.g., representing test and control cells), each labeled with a different fluorophore, are hybridized to a single array for the purpose of identifying genes that are differentially expressed, the calibration is done by labeling samples of the calibrating cDNA with the two fluorophores and adding identical amounts of each to the hybridization mixture.

The output of the photomultiplier tube is digitized using a 12-bit RTI-835H analog-to-digital (A/D) conversion board (Analog Devices, Inc., Norwood, MA) installed in an IBM-compatible PC computer. The digitized data are displayed as an image where the signal intensity is mapped using a linear 20-color transformation to a pseudocolor scale ranging from blue (low signal) to red (high signal). The data is also analyzed quantitatively. Where two different fluorophores are excited and measured simultaneously, the data are first corrected for optical crosstalk (due to overlapping emission spectra) between the fluorophores using each fluorophore's emission spectrum.

A grid is superimposed over the fluorescence signal image such that the signal from each spot is centered in each element of the grid. The fluorescence signal within each element is then integrated to obtain a numerical value corresponding to the average intensity of the signal. The software used for signal analysis is the GEMTOOLS gene expression analysis program (Incyte).

XII. Complementary Nucleic Acids

Sequences complementary to the sptm are used to detect, decrease, or inhibit expression of the naturally occurring nucleotide. The use of oligonucleotides comprising from about 15 to 30 base pairs is typical in the art. However, smaller or larger sequence fragments can also be used. Appropriate oligonucleotides are designed from the sptm using OLIGO 4.06 software (National Biosciences) or other appropriate programs and are synthesized using methods standard in the art or

ordered from a commercial supplier. To inhibit transcription, a complementary oligonucleotide is designed from the most unique 5' sequence and used to prevent transcription factor binding to the promoter sequence. To inhibit translation, a complementary oligonucleotide is designed to prevent ribosomal binding and processing of the transcript.

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XIII. Expression of SPTM

Expression and purification of SPTM is accomplished using bacterial or virus-based expression systems. For expression of SPTM in bacteria, cDNA is subcloned into an appropriate vector containing an antibiotic resistance gene and an inducible promoter that directs high levels of
10 cDNA transcription. Examples of such promoters include, but are not limited to, the *trp-lac* (*tac*) hybrid promoter and the T5 or T7 bacteriophage promoter in conjunction with the *lac* operator regulatory element. Recombinant vectors are transformed into suitable bacterial hosts, e.g., BL21(DE3). Antibiotic resistant bacteria express SPTM upon induction with isopropyl beta-D-thiogalactopyranoside (IPTG). Expression of SPTM in eukaryotic cells is achieved by infecting
15 insect or mammalian cell lines with recombinant Autographica californica nuclear polyhedrosis virus (AcMNPV), commonly known as baculovirus. The nonessential polyhedrin gene of baculovirus is replaced with cDNA encoding SPTM by either homologous recombination or bacterial-mediated transposition involving transfer plasmid intermediates. Viral infectivity is maintained and the strong polyhedrin promoter drives high levels of cDNA transcription. Recombinant baculovirus is used to
20 infect Spodoptera frugiperda (Sf9) insect cells in most cases, or human hepatocytes, in some cases. Infection of the latter requires additional genetic modifications to baculovirus. (See e.g., Engelhard, supra; and Sandig, supra.)

In most expression systems, SPTM is synthesized as a fusion protein with, e.g., glutathione S-transferase (GST) or a peptide epitope tag, such as FLAG or 6-His, permitting rapid, single-step,
25 affinity-based purification of recombinant fusion protein from crude cell lysates. GST, a 26-kilodalton enzyme from Schistosoma japonicum, enables the purification of fusion proteins on immobilized glutathione under conditions that maintain protein activity and antigenicity (Amersham Pharmacia Biotech). Following purification, the GST moiety can be proteolytically cleaved from SPTM at specifically engineered sites. FLAG, an 8-amino acid peptide, enables immunoaffinity
30 purification using commercially available monoclonal and polyclonal anti-FLAG antibodies (Eastman Kodak Company, Rochester NY). 6-His, a stretch of six consecutive histidine residues, enables purification on metal-chelate resins (QIAGEN). Methods for protein expression and purification are discussed in Ausubel (1995, supra, Chapters 10 and 16). Purified SPTM obtained by these methods can be used directly in the following activity assay.

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XIV. Demonstration of SPTM Activity

An assay for SPTM activity measures the expression of SPTM on the cell surface. cDNA encoding SPTM is subcloned into an appropriate mammalian expression vector suitable for high levels of cDNA expression. The resulting construct is transfected into a nonhuman cell line such as NIH3T3. Cell surface proteins are labeled with biotin using methods known in the art. Immunoprecipitations are performed using SPTM-specific antibodies, and immunoprecipitated samples are analyzed using SDS-PAGE and immunoblotting techniques. The ratio of labeled immunoprecipitant to unlabeled immunoprecipitant is proportional to the amount of SPTM expressed on the cell surface.

Alternatively, an assay for SPTM activity measures the amount of SPTM in secretory, membrane-bound organelles. Transfected cells as described above are harvested and lysed. The lysate is fractionated using methods known to those of skill in the art, for example, sucrose gradient ultracentrifugation. Such methods allow the isolation of subcellular components such as the Golgi apparatus, ER, small membrane-bound vesicles, and other secretory organelles. Immunoprecipitations from fractionated and total cell lysates are performed using SPTM-specific antibodies, and immunoprecipitated samples are analyzed using SDS-PAGE and immunoblotting techniques. The concentration of SPTM in secretory organelles relative to SPTM in total cell lysate is proportional to the amount of SPTM in transit through the secretory pathway.

XV. Functional Assays

SPTM function is assessed by expressing sptm at physiologically elevated levels in mammalian cell culture systems. cDNA is subcloned into a mammalian expression vector containing a strong promoter that drives high levels of cDNA expression. Vectors of choice include pCMV SPORT (Life Technologies) and pCR3.1 (Invitrogen Corporation, Carlsbad CA), both of which contain the cytomegalovirus promoter. 5-10 μg of recombinant vector are transiently transfected into a human cell line, preferably of endothelial or hematopoietic origin, using either liposome formulations or electroporation. 1-2 μg of an additional plasmid containing sequences encoding a marker protein are co-transfected.

Expression of a marker protein provides a means to distinguish transfected cells from nontransfected cells and is a reliable predictor of cDNA expression from the recombinant vector. Marker proteins of choice include, e.g., Green Fluorescent Protein (GFP; CLONTECH), CD64, or a CD64-GFP fusion protein. Flow cytometry (FCM), an automated laser optics-based technique, is used to identify transfected cells expressing GFP or CD64-GFP and to evaluate the apoptotic state of the cells and other cellular properties.

FCM detects and quantifies the uptake of fluorescent molecules that diagnose events preceding or coincident with cell death. These events include changes in nuclear DNA content as

measured by staining of DNA with propidium iodide; changes in cell size and granularity as measured by forward light scatter and 90 degree side light scatter; down-regulation of DNA synthesis as measured by decrease in bromodeoxyuridine uptake; alterations in expression of cell surface and intracellular proteins as measured by reactivity with specific antibodies; and alterations in plasma membrane composition as measured by the binding of fluorescein-conjugated Annexin V protein to the cell surface. Methods in flow cytometry are discussed in Ormerod, M. G. (1994) Flow Cytometry, Oxford, New York NY.

The influence of SPTM on gene expression can be assessed using highly purified populations of cells transfected with sequences encoding SPTM and either CD64 or CD64-GFP. CD64 and CD64-GFP are expressed on the surface of transfected cells and bind to conserved regions of human immunoglobulin G (IgG). Transfected cells are efficiently separated from nontransfected cells using magnetic beads coated with either human IgG or antibody against CD64 (DYNAL, Inc., Lake Success NY). mRNA can be purified from the cells using methods well known by those of skill in the art. Expression of mRNA encoding SPTM and other genes of interest can be analyzed by northern analysis or microarray techniques.

XVI. Production of Antibodies

SPTM substantially purified using polyacrylamide gel electrophoresis (PAGE; see, e.g., Harrington, M.G. (1990) Methods Enzymol. 182:488-495), or other purification techniques, is used to immunize rabbits and to produce antibodies using standard protocols.

Alternatively, the SPTM amino acid sequence is analyzed using LASERGENE software (DNASTAR) to determine regions of high immunogenicity, and a corresponding peptide is synthesized and used to raise antibodies by means known to those of skill in the art. Methods for selection of appropriate epitopes, such as those near the C-terminus or in hydrophilic regions are well described in the art. (See, e.g., Ausubel, 1995, supra, Chapter 11.)

Typically, peptides 15 residues in length are synthesized using an ABI 431A peptide synthesizer (PE Biosystems) using fmoc-chemistry and coupled to KLH (Sigma) by reaction with N-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS) to increase immunogenicity. (See, e.g., Ausubel, supra.) Rabbits are immunized with the peptide-KLH complex in complete Freund's adjuvant. Resulting antisera are tested for antipeptide activity by, for example, binding the peptide to plastic, blocking with 1% BSA, reacting with rabbit antisera, washing, and reacting with radio-iodinated goat anti-rabbit IgG. Antisera with antipeptide activity are tested for anti-SPTM activity using protocols well known in the art, including ELISA, RIA, and immunoblotting.

XVII. Purification of Naturally Occurring SPTM Using Specific Antibodies

Naturally occurring or recombinant SPTM is substantially purified by immunoaffinity chromatography using antibodies specific for SPTM. An immunoaffinity column is constructed by covalently coupling anti-SPTM antibody to an activated chromatographic resin, such as CNBr-activated SEPHAROSE (Amersham Pharmacia Biotech). After the coupling, the resin is blocked and washed according to the manufacturer's instructions.

Media containing SPTM are passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of SPTM (e.g., high ionic strength buffers in the presence of detergent). The column is eluted under conditions that disrupt antibody/SPTM binding (e.g., a buffer of pH 2 to pH 3, or a high concentration of a chaotrope, such as urea or thiocyanate ion), and SPTM is collected.

XVIII. Identification of Molecules Which Interact with SPTM

SPTM, or biologically active fragments thereof, are labeled with ^{125}I Bolton-Hunter reagent. (See, e.g., Bolton, A.E. and W.M. Hunter (1973) Biochem. J. 133:529-539.) Candidate molecules previously arrayed in the wells of a multi-well plate are incubated with the labeled SPTM, washed, and any wells with labeled SPTM complex are assayed. Data obtained using different concentrations of SPTM are used to calculate values for the number, affinity, and association of SPTM with the candidate molecules.

Alternatively, molecules interacting with SPTM are analyzed using the yeast two-hybrid system as described in Fields, S. and O. Song (1989) Nature 340:245-246, or using commercially available kits based on the two-hybrid system, such as the MATCHMAKER system (CLONTECH).

SPTM may also be used in the PATHCALLING process (CuraGen Corp., New Haven CT) which employs the yeast two-hybrid system in a high-throughput manner to determine all interactions between the proteins encoded by two large libraries of genes (Nandabalan, K. et al. (2000) U.S. Patent No. 6,057,101).

All publications and patents mentioned in the above specification are herein incorporated by reference. Various modifications and variations of the described method and system of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with specific preferred embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the above-described modes for carrying out the invention which are obvious to those skilled in the field of molecular biology or related fields are intended to be within the scope of the following claims.

TABLE 1

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
1	1978.1	g6807999	2.00E-32	Homo sapiens mRNA; cDNA DKFZp761K1824 (from clone DKFZp761K1824).
2	2588.4	g1947111	6.00E-26	B0041.5 gene product (Caenorhabditis elegans)
3	201759.3	g4929566	0	Homo sapiens CGI-49 protein mRNA, complete cds.
4	208184.1	g6690196	0	Homo sapiens clone HQ0270.
5	212029.3	g5923798	1.00E-18	Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.
6	213446.2	g1707057	4.00E-76	coded for by C. elegans cDNA CEESS55F; coded for by C. elegans cDNA yk84a1.3; coded for by C. elegans cDNA yk78g7.3; coded for by C. elegans cDNA yk168g9.5; coded for by C. elegans cDNA yk78g7.5; coded for by C. elegans cDNA yk84a1.5; strong s ()
7	228864.4	g5656743	1.00E-120	Supported by Human EST H08032.1 (NID:g872854), mouse EST AA870042.1 (NID:g2965487), and genscan (Homo sapiens)
8	229840.3	g5817280	1.00E-91	conserved hypothetical protein (Schizosaccharomyces pombe)
9	231793.2	g1665801	2.00E-73	KIAA0281 (Homo sapiens)
10	234137.5	g6759520	0	Novel human gene mapping to chomosome 1.
11	234671.14	g3152704	1.00E-48	Homo sapiens COBW-like placental protein mRNA, partial cds.
12	241236.3	g1707258	7.00E-13	C17H11.6 gene product (Caenorhabditis elegans)
13	245014.1	g4406631	9.00E-17	Homo sapiens clone 25221 mRNA sequence, complete cds.
14	245251.6	g4689149	0	Homo sapiens PTD001 mRNA, complete cds.
15	252875.1	g6706666	0	dJ234P15.3 (novel protein similar to (predicted) yeast and worm proteins) (Homo sapiens)
16	252964.2	g6560611	0	Homo sapiens PRO0461 mRNA, complete cds.
17	267153.7	g4886492	0	Homo sapiens mRNA; cDNA DKFZp564A032 (from clone DKFZp564A032); complete cds.
18	331244.6	g4929598	0	Homo sapiens CGI-65 protein mRNA, complete cds.
19	335484.1	g3879914	1.00E-76	predicted using Genefinder; cDNA EST EMBL:C13850 comes from this gene; cDNA EST EMBL:C11575 comes from this gene; cDNA EST yk343f4.5 comes from this gene (Caenorhabditis elegans)
20	337489.2	g6650611	0	Homo sapiens Ran binding protein 11 mRNA, complete cds.
21	359574.5	g707086	6.00E-24	unknown protein (Bacillus subtilis)
22	360645.5	g3947589	2.00E-48	cDNA EST yk255b9.3 comes from this gene; cDNA EST yk255b9.5 comes from this gene; cDNA EST EMBL:M75923 comes from this gene (Caenorhabditis elegans)
23	404145.7	g4589529	0	Homo sapiens mRNA for KIAA0943 protein, partial cds.

TABLE 1

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
24	480119.1	g4884352	0	Homo sapiens mRNA; cDNA DKFZp586O031 (from clone DKFZp586O031).
25	480951.5	g5713280	0	Homo sapiens Yippee protein mRNA, partial cds.
26	481257.3	g4929600	0	Homo sapiens CGI-66 protein mRNA, complete cds.

TABLE 2

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type
1	1978.1	401	478	forward 2	TM
2	2588.4	362	454	forward 2	SP
2	2588.4	1552	1626	forward 1	TM
3	201759.3	926	1009	forward 2	SP
4	208184.1	1438	1533	forward 1	SP
4	208184.1	159	242	forward 3	SP
4	208184.1	1194	1271	forward 3	TM
5	212029.3	128	208	forward 2	SP
6	213446.2	944	1021	forward 2	SP
6	213446.2	614	718	forward 2	SP
6	213446.2	934	1020	forward 1	TM
7	228864.4	1600	1680	forward 1	SP
7	228864.4	116	229	forward 2	SP
7	228864.4	543	638	forward 3	SP
8	229840.3	2861	2938	forward 2	TM
9	231793.2	730	810	forward 1	SP
10	234137.5	708	806	forward 3	SP
11	234671.14	557	634	forward 2	TM
12	241236.3	1397	1501	forward 2	SP
13	245014.1	1326	1412	forward 3	TM
14	245251.6	826	909	forward 1	SP
15	252875.1	2388	2468	forward 3	TM
16	252964.2	2954	3037	forward 2	TM
17	267153.7	746	829	forward 2	SP
18	331244.6	413	493	forward 2	TM
19	335484.1	1977	2060	forward 3	TM
19	335484.1	2805	2888	forward 3	TM
20	337489.2	666	746	forward 3	TM
21	359574.5	2571	2657	forward 3	SP
21	359574.5	1845	1931	forward 3	SP
21	359574.5	1665	1760	forward 3	SP
22	360645.5	415	495	forward 1	SP
23	404145.7	2141	2248	forward 2	SP
23	404145.7	666	785	forward 3	SP
24	480119.1	1181	1267	forward 2	SP
24	480119.1	413	499	forward 2	SP
25	480951.5	2523	2606	forward 3	TM
26	481257.3	2774	2860	forward 2	TM

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
1	1978.1	g1855482	1	217
1	1978.1	3137104H1	1	272
1	1978.1	3137104F6	1	381
1	1978.1	3526040H1	11	304
1	1978.1	3523774H1	11	357
1	1978.1	g1267790	148	605
1	1978.1	g1267782	148	522
1	1978.1	g1958606	164	580
1	1978.1	3031854H1	269	571
1	1978.1	4832441H1	339	597
1	1978.1	g1775794	353	418
1	1978.1	4142134H1	553	758
1	1978.1	1600481H1	605	800
1	1978.1	1600481F6	605	966
1	1978.1	4379163H1	653	915
1	1978.1	2901551H1	668	927
1	1978.1	1678677H1	677	909
1	1978.1	3842809H1	736	1043
1	1978.1	1793709H1	755	1050
1	1978.1	2773028H1	755	1009
1	1978.1	3602828H1	860	1155
1	1978.1	1610720H1	934	1142
1	1978.1	2366358H1	976	1193
1	1978.1	5497064H1	1036	1265
1	1978.1	3742273H1	1063	1273
1	1978.1	5261375H1	1113	1334
1	1978.1	1378352F1	1149	1688
1	1978.1	1378352H1	1149	1386
1	1978.1	1281776F6	1190	1796
1	1978.1	1281776H1	1190	1453
1	1978.1	2097593H1	1199	1380
1	1978.1	2098893H1	1199	1445
1	1978.1	g714966	1208	1550
1	1978.1	3929766H1	1219	1504
1	1978.1	g1425881	1230	1639
1	1978.1	g989565	1249	1465
1	1978.1	1369088H1	1249	1478
1	1978.1	627100H1	1249	1491
1	1978.1	815413H1	1269	1522
1	1978.1	4505379H1	1271	1473
1	1978.1	1281776T6	1348	1957
1	1978.1	g1860340	1388	1801
1	1978.1	g1959763	1438	1931
1	1978.1	1600481T6	1439	1962
1	1978.1	3137104T6	1467	1961
1	1978.1	g3231943	1542	1999
1	1978.1	5195075H1	1543	1772
1	1978.1	g3231851	1547	1999
1	1978.1	g3539313	1559	2000
1	1978.1	g3539311	1559	2001

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
1	1978.1	764088H1	1571	1866
1	1978.1	765817H1	1571	1820
1	1978.1	765817R6	1571	1972
1	1978.1	765817T6	1571	1964
1	1978.1	g1860995	1588	2012
1	1978.1	g4068873	1592	2000
1	1978.1	g2787512	1594	2000
1	1978.1	g1202822	1605	2000
1	1978.1	g1425795	1639	2004
1	1978.1	2202630T6	1656	1956
1	1978.1	2202630H1	1664	1911
1	1978.1	2202630F6	1664	1996
1	1978.1	g1775688	1702	1969
1	1978.1	g714967	1724	2012
1	1978.1	2290116H1	1725	1992
1	1978.1	2127226H1	1725	1998
1	1978.1	3815472H1	1739	2000
1	1978.1	g989478	1752	1987
1	1978.1	g3043215	1787	2005
1	1978.1	2413731H1	1868	2004
2	2588.4	3502438H1	2224	2533
2	2588.4	g2786213	2248	2674
2	2588.4	g3277689	2254	2669
2	2588.4	2366762H1	2248	2486
2	2588.4	1910722H1	2255	2499
2	2588.4	g4286541	2256	2664
2	2588.4	g3052444	2260	2670
2	2588.4	832051T6	2268	2624
2	2588.4	g2873700	2274	2671
2	2588.4	g2876032	2276	2668
2	2588.4	2663178H1	2278	2519
2	2588.4	g1482457	2282	2670
2	2588.4	2868714H1	2290	2577
2	2588.4	g3239166	2301	2671
2	2588.4	g3700567	2302	2669
2	2588.4	4595434H1	2361	2549
2	2588.4	g1118566	2382	2669
2	2588.4	g1693563	2384	2670
2	2588.4	g1920095	2390	2675
2	2588.4	2370688H1	2416	2519
2	2588.4	g1952447	2420	2676
2	2588.4	g1124041	2428	2669
2	2588.4	g787440	2432	2669
2	2588.4	g2322889	2432	2803
2	2588.4	g1885881	2434	2677
2	2588.4	g1267377	2451	2817
2	2588.4	g1119118	2466	2669
2	2588.4	g1218402	2474	2669
2	2588.4	276858OT6	2481	2630
2	2588.4	g2102824	2482	2892

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
2	2588.4	1844326H1	2483	2669
2	2588.4	2768580H1	2488	2670
2	2588.4	2768580F6	2488	2670
2	2588.4	g2457806	2514	2667
2	2588.4	1854244H1	2530	2669
2	2588.4	1830904T6	2533	2622
2	2588.4	1854244T6	2533	2630
2	2588.4	g1484958	2560	2670
2	2588.4	3565846H1	2565	2885
2	2588.4	g845861	2570	2688
2	2588.4	2094684H1	2574	2669
2	2588.4	4157557H1	2598	2867
2	2588.4	3412843H1	2640	2859
2	2588.4	2467396T6	2734	3206
2	2588.4	2467396F6	2741	3192
2	2588.4	2467396H1	2741	2978
2	2588.4	3148660H1	2882	2992
2	2588.4	g2435914	2884	3178
2	2588.4	2832630F6	2918	3237
2	2588.4	2832630H1	2918	3174
2	2588.4	2832630T6	2922	3199
2	2588.4	g1154518	2999	3296
2	2588.4	g845812	3031	3245
2	2588.4	4118483H1	3044	3213
2	2588.4	g1123141	3054	3244
2	2588.4	2268209T6	761	1105
2	2588.4	2672328F6	1	357
2	2588.4	2590094H2	1	227
2	2588.4	2672328H1	1	227
2	2588.4	2672248H1	1	227
2	2588.4	2159193H1	1	149
2	2588.4	2660709H1	5	253
2	2588.4	3046945H1	14	316
2	2588.4	2047661H1	30	315
2	2588.4	g1957845	31	476
2	2588.4	g2210487	57	387
2	2588.4	3698574H1	308	459
2	2588.4	5633547H1	440	637
2	2588.4	2892108H1	440	708
2	2588.4	3496131H1	490	777
2	2588.4	3111455H1	513	783
2	2588.4	2536480H1	550	792
2	2588.4	4971550H1	560	817
2	2588.4	2268209R6	570	955
2	2588.4	2268209H1	571	833
2	2588.4	1259305F1	611	1189
2	2588.4	3773508H1	612	930
2	2588.4	1259305H1	611	838
2	2588.4	825346H1	685	983
2	2588.4	2122376H1	702	955

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
2	2588.4	3108360H1	743	1017
2	2588.4	g2210429	769	1039
2	2588.4	5188115H1	895	1068
2	2588.4	646258H1	907	1068
2	2588.4	4564951H1	961	1217
2	2588.4	661278H1	999	1263
2	2588.4	660712H1	999	1267
2	2588.4	634487H1	987	1238
2	2588.4	g2037676	1040	1244
2	2588.4	5035180H1	1074	1347
2	2588.4	661278R6	999	1563
2	2588.4	5035211H1	1074	1324
2	2588.4	g1523090	1093	1462
2	2588.4	3523389H1	1113	1352
2	2588.4	g1192612	1099	1470
2	2588.4	1450413H1	1129	1376
2	2588.4	4346111H1	1138	1389
2	2588.4	4346627H1	1138	1401
2	2588.4	3174422H1	1139	1381
2	2588.4	2645913H1	1158	1420
2	2588.4	4959350H1	1163	1408
2	2588.4	2632516H1	1170	1408
2	2588.4	2995782H1	1187	1446
2	2588.4	g1950525	1257	1594
2	2588.4	5501962H1	1295	1527
2	2588.4	2866753H1	1313	1647
2	2588.4	g1920346	1372	1779
2	2588.4	g1950552	1426	1678
2	2588.4	1990742H1	1432	1677
2	2588.4	g2102880	1453	1926
2	2588.4	2108316H1	1491	1762
2	2588.4	4323533H1	1493	1761
2	2588.4	2326875H1	1498	1749
2	2588.4	2326664H1	1498	1726
2	2588.4	5117484H1	1534	1793
2	2588.4	1794995H1	1560	1832
2	2588.4	3203064H1	1561	1846
2	2588.4	2406583H1	1576	1709
2	2588.4	4144701H1	1594	1773
2	2588.4	3605515H1	1621	1861
2	2588.4	2715994H1	1641	1885
2	2588.4	3141136H1	1644	1889
2	2588.4	3687001H1	1650	1947
2	2588.4	g900018	1654	1998
2	2588.4	g1639521	1672	1916
2	2588.4	2860261H1	1690	1969
2	2588.4	3254658H1	1699	1932
2	2588.4	3095495H1	1712	1995
2	2588.4	2660751H1	1768	2016
2	2588.4	832051R6	1804	2094

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
2	2588.4	1812964H1	1804	2036
2	2588.4	832051H1	1804	2072
2	2588.4	1812964F6	1805	2328
2	2588.4	2900724H1	1812	2115
2	2588.4	1496448H1	1817	2058
2	2588.4	g2912624	1840	2122
2	2588.4	g2879636	1844	2122
2	2588.4	g2191548	1846	2122
2	2588.4	5506884H1	1863	2096
2	2588.4	2203126H1	1903	2157
2	2588.4	4159080H1	1906	2135
2	2588.4	1857148H1	1916	2161
2	2588.4	5099926H1	1925	2212
2	2588.4	g787181	1953	2177
2	2588.4	3327731H1	1983	2283
2	2588.4	5572386H1	1994	2106
2	2588.4	4986441H1	2004	2303
2	2588.4	3110534H1	2004	2279
2	2588.4	5396265T1	2047	2631
2	2588.4	2189071T6	2070	2626
2	2588.4	2189071H1	2072	2357
2	2588.4	2189071F6	2072	2492
2	2588.4	2783063H1	2074	2365
2	2588.4	5396375T1	2081	2633
2	2588.4	4862535H1	2082	2244
2	2588.4	2672328T6	2092	2636
2	2588.4	1972459H1	2094	2376
2	2588.4	3786773H1	2114	2409
2	2588.4	661278T6	2145	2631
2	2588.4	3994175H1	2158	2450
2	2588.4	3995990H1	2160	2411
2	2588.4	5137950H2	2208	2487
2	2588.4	g1523038	2213	2669
2	2588.4	2664705H1	2212	2338
2	2588.4	g3308729	2218	2673
3	201759.3	836624R1	823	1315
3	201759.3	039821H1	861	1031
3	201759.3	5278457H1	871	1132
3	201759.3	836624H1	872	1143
3	201759.3	836632H1	873	1140
3	201759.3	4299787H1	879	1057
3	201759.3	263784H1	898	1265
3	201759.3	g2017411	900	1347
3	201759.3	826199R1	904	1553
3	201759.3	826199H1	904	1190
3	201759.3	g1463426	908	1456
3	201759.3	2011073H1	914	1130
3	201759.3	4203594H1	917	1203
3	201759.3	2021844H1	918	1180
3	201759.3	4861150H1	919	1199

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
3	201759.3	1494424H1	958	1173
3	201759.3	3697752H1	970	1290
3	201759.3	g1049651	984	1332
3	201759.3	3015055H1	987	1320
3	201759.3	1857956H1	990	1165
3	201759.3	1857956F6	990	1530
3	201759.3	5112648H1	997	1334
3	201759.3	535858H1	1000	1099
3	201759.3	5091726H1	1015	1322
3	201759.3	1952952H1	1015	1309
3	201759.3	1257476H1	1016	1281
3	201759.3	4585955H1	1017	1309
3	201759.3	5836690H1	1018	1270
3	201759.3	4648947H1	1027	1197
3	201759.3	958699H1	1029	1339
3	201759.3	3960850H2	1028	1325
3	201759.3	691887H1	1030	1258
3	201759.3	g1240155	1040	1284
3	201759.3	g1025462	1053	1335
3	201759.3	g1264434	1053	1450
3	201759.3	3354080H1	1065	1243
3	201759.3	g863516	1067	1324
3	201759.3	5428281H1	1073	1362
3	201759.3	1236418H1	1075	1290
3	201759.3	3525638H1	1085	1444
3	201759.3	4086966H1	1102	1398
3	201759.3	2921953H1	1116	1433
3	201759.3	2370849H1	1117	1402
3	201759.3	1649210H1	1117	1383
3	201759.3	4159589H1	1126	1416
3	201759.3	g3919705	1134	1658
3	201759.3	2840735H1	1139	1417
3	201759.3	1401895H1	1140	1414
3	201759.3	g2110825	1140	1652
3	201759.3	3807071H1	1141	1491
3	201759.3	4112417H1	1144	1251
3	201759.3	3843828H1	1143	1465
3	201759.3	g3238572	1144	1668
3	201759.3	g2347672	1147	1665
3	201759.3	g2930046	1147	1665
3	201759.3	g3238573	1150	1668
3	201759.3	g2742072	1171	1658
3	201759.3	g3595471	1176	1658
3	201759.3	g3988715	1176	1658
3	201759.3	g3644962	1177	1668
3	201759.3	3466714H1	1177	1467
3	201759.3	g1384561	1180	1673
3	201759.3	g3446683	1181	1670
3	201759.3	g3679958	1184	1664
3	201759.3	g1332165	1190	1663

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
3	201759.3	3600088H1	1200	1528
3	201759.3	254256IT6	1207	1633
3	201759.3	900346H1	1225	1325
3	201759.3	900346R1	1225	1658
3	201759.3	g848629	1225	1571
3	201759.3	5056168H1	1225	1530
3	201759.3	3112117H1	1233	1546
3	201759.3	g2524963	1240	1658
3	201759.3	g4332204	1241	1665
3	201759.3	3366929H1	1244	1517
3	201759.3	g3432662	1244	1666
3	201759.3	g2806722	1246	1661
3	201759.3	g3931304	1247	1667
3	201759.3	g3601403	1248	1663
3	201759.3	g3238932	1252	1665
3	201759.3	g3931309	1258	1667
3	201759.3	2293916H1	1261	1529
3	201759.3	2399275H1	1272	1541
3	201759.3	g2557656	1281	1663
3	201759.3	g2617892	1281	1659
3	201759.3	g2463986	1286	1668
3	201759.3	g2457535	1288	1646
3	201759.3	g3416543	1292	1643
3	201759.3	g3095258	1297	1665
3	201759.3	g2669541	1297	1658
3	201759.3	3467486H1	1311	1579
3	201759.3	g2198192	1314	1665
3	201759.3	g749662	1313	1659
3	201759.3	g752157	1313	1580
3	201759.3	g2188331	1324	1670
3	201759.3	g3308655	1325	1658
3	201759.3	g2156163	1331	1835
3	201759.3	g3229304	1342	1668
3	201759.3	g2969733	1349	1665
3	201759.3	266449IT6	1352	1622
3	201759.3	g1049959	1369	1670
3	201759.3	g2243211	1366	1668
3	201759.3	g863517	1371	1642
3	201759.3	g784617	1372	1665
3	201759.3	g1614677	1368	1658
3	201759.3	g4148476	1369	1665
3	201759.3	g1294977	1369	1658
3	201759.3	g2955119	1373	1667
3	201759.3	g1448860	1373	1658
3	201759.3	g2958161	1395	1658
3	201759.3	g3233016	1401	1663
3	201759.3	4640182H1	1401	1660
3	201759.3	g3884622	1404	1670
3	201759.3	g3431226	1406	1658
3	201759.3	g3843156	1407	1658

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
3	201759.3	2101118H1	1413	1655
3	201759.3	2044357H1	1428	1688
3	201759.3	3573519T6	1432	1996
3	201759.3	1695963T6	1432	1995
3	201759.3	2351137H1	1458	1662
3	201759.3	1901951H1	1468	1763
3	201759.3	2505488H2	1468	1721
3	201759.3	2052204H1	1486	1761
3	201759.3	2016130H1	1	95
3	201759.3	5373386H1	24	184
3	201759.3	6026840H1	51	139
3	201759.3	2598924H1	87	375
3	201759.3	2598924F6	88	598
3	201759.3	1318607H1	88	321
3	201759.3	3450621H1	93	257
3	201759.3	2664494H1	96	332
3	201759.3	2664494F6	96	652
3	201759.3	3573519F6	98	681
3	201759.3	3573519H1	98	405
3	201759.3	4177617H1	102	371
3	201759.3	4920283H1	101	194
3	201759.3	4843441H1	104	378
3	201759.3	3069036H1	104	395
3	201759.3	3374007H1	109	376
3	201759.3	4662762H1	109	366
3	201759.3	2160985H1	109	364
3	201759.3	2964373H1	109	423
3	201759.3	3561542H1	110	405
3	201759.3	3579440H1	110	414
3	201759.3	1571030H1	110	302
3	201759.3	3595416H1	112	234
3	201759.3	2133581H1	113	395
3	201759.3	3281108H1	112	376
3	201759.3	3658478H1	112	394
3	201759.3	3359378H1	117	395
3	201759.3	g1962636	119	523
3	201759.3	3373501H1	119	374
3	201759.3	899120H1	123	209
3	201759.3	2913242H1	123	383
3	201759.3	4974963H1	123	215
3	201759.3	g1813092	125	514
3	201759.3	1531710H1	126	327
3	201759.3	4270743H1	163	428
3	201759.3	4522315H1	170	429
3	201759.3	2647741H1	176	428
3	201759.3	3031088H1	194	497
3	201759.3	g2163335	192	565
3	201759.3	3895133H1	205	527
3	201759.3	3950958H1	272	434
3	201759.3	5538554H2	305	502

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
3	201759.3	1911718H1	323	482
3	201759.3	g4084676	346	828
3	201759.3	5713320H1	362	659
3	201759.3	5836526H1	363	651
3	201759.3	5833621H1	363	651
3	201759.3	2858391H1	367	631
3	201759.3	2859193H1	367	622
3	201759.3	g2255078	377	819
3	201759.3	2730576H1	423	698
3	201759.3	1695963F6	433	907
3	201759.3	4548639H1	433	676
3	201759.3	2674195H1	433	678
3	201759.3	1695963H1	433	685
3	201759.3	g2163176	461	890
3	201759.3	3422493H1	470	700
3	201759.3	597747H1	475	712
3	201759.3	436190H1	489	747
3	201759.3	g761512	496	878
3	201759.3	g1799100	496	1022
3	201759.3	1707486H1	506	730
3	201759.3	3758616H1	511	639
3	201759.3	173498H1	523	720
3	201759.3	g883464	549	959
3	201759.3	4299747H1	566	794
3	201759.3	4301171H1	566	775
3	201759.3	g788509	576	853
3	201759.3	3968576H1	586	911
3	201759.3	173498F1	593	1035
3	201759.3	3624367H1	611	886
3	201759.3	5811130H1	618	916
3	201759.3	2480172H1	620	957
3	201759.3	3233075H1	626	934
3	201759.3	1376454H1	629	872
3	201759.3	1376454F1	629	1103
3	201759.3	4824995H1	633	903
3	201759.3	1611033H1	638	856
3	201759.3	1611064H1	638	840
3	201759.3	850649R1	639	1297
3	201759.3	850649H1	639	901
3	201759.3	280397H1	640	1029
3	201759.3	3608679H1	639	848
3	201759.3	3502463H1	644	966
3	201759.3	4302480H1	646	950
3	201759.3	166390H1	652	925
3	201759.3	465154H1	675	922
3	201759.3	2471187H1	696	946
3	201759.3	g1332164	698	1205
3	201759.3	g1988555	704	1008
3	201759.3	167885H1	704	1055
3	201759.3	167849H1	705	1059

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
3	201759.3	087337H1	707	954
3	201759.3	1482767H1	724	988
3	201759.3	g1614676	733	862
3	201759.3	g874674	740	1147
3	201759.3	g877795	740	1099
3	201759.3	668420H1	739	986
3	201759.3	061003H1	741	915
3	201759.3	g1448859	753	1297
3	201759.3	5861969H1	754	1038
3	201759.3	2961324H1	754	1072
3	201759.3	2545528H1	760	1023
3	201759.3	030800H1	761	1060
3	201759.3	3599778H1	779	1014
3	201759.3	4886074H1	790	1073
3	201759.3	2702328H1	790	1054
3	201759.3	4724311H1	797	910
3	201759.3	1674833H1	802	1024
3	201759.3	g1055891	803	1147
3	201759.3	4425751H1	817	1097
3	201759.3	700809H1	819	1111
3	201759.3	700858H1	819	1108
3	201759.3	g1406784	1492	1915
3	201759.3	g3307726	1501	1658
3	201759.3	g3405773	1505	1969
3	201759.3	1007491H1	1541	1848
3	201759.3	g3841579	1547	1665
3	201759.3	5906115H1	1549	1665
3	201759.3	g3016169	1550	1658
3	201759.3	g2967986	1558	1658
3	201759.3	1416494H1	1560	1811
3	201759.3	2111952H1	1560	1859
3	201759.3	g2265647	1572	2043
3	201759.3	g2106597	1571	1674
3	201759.3	040426H1	1577	1834
3	201759.3	g314936	1600	2038
3	201759.3	g3872004	1609	2038
3	201759.3	g2112437	1613	2047
3	201759.3	g1382965	1616	2039
3	201759.3	g2930234	1617	2039
3	201759.3	g2559360	1619	2038
3	201759.3	1602514T6	1630	1972
3	201759.3	5022224H1	1637	1919
3	201759.3	1602514F6	1638	1821
3	201759.3	1602514H1	1638	1841
3	201759.3	g1813014	1642	2039
3	201759.3	g2107167	1647	2047
3	201759.3	1857956T6	1653	2000
3	201759.3	g3770498	1655	2040
3	201759.3	g518019	1702	2038
3	201759.3	g883358	1708	2046

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
3	201759.3	g678008	1717	2038
3	201759.3	g3777972	1726	2041
3	201759.3	1655510T6	1743	1998
3	201759.3	1655510H1	1751	2003
3	201759.3	1655502H1	1751	1999
3	201759.3	g1211514	1750	2039
3	201759.3	1655510F6	1751	2038
3	201759.3	g4270201	1753	2046
3	201759.3	g1025463	1758	2033
3	201759.3	2410391H1	1760	1986
3	201759.3	4565053H1	1763	2014
3	201759.3	g874588	1768	2062
3	201759.3	g2836530	1783	2039
3	201759.3	g2620460	1787	2038
3	201759.3	5022224T1	1794	1995
3	201759.3	g848545	1797	2010
3	201759.3	g2269911	1826	2038
3	201759.3	g1202659	1857	2052
3	201759.3	5597773H1	1869	2043
3	201759.3	g869167	1874	2062
3	201759.3	1818223H1	1896	2045
3	201759.3	g2658131	1898	2347
3	201759.3	g3595015	1910	2346
3	201759.3	5059857H1	1942	2004
3	201759.3	4654185H1	1959	2242
3	201759.3	3489630H1	1968	2039
3	201759.3	g750011	2022	2358
3	201759.3	g4194527	2035	2346
3	201759.3	g3843200	2039	2347
3	201759.3	g2658236	2054	2347
3	201759.3	2844058F6	2078	2347
3	201759.3	2844058H1	2078	2350
3	201759.3	g752055	2137	2322
3	201759.3	g3433471	2136	2345
4	208184.1	5329975H1	1526	1795
4	208184.1	3962839H1	1531	1848
4	208184.1	3963078H1	1531	1837
4	208184.1	832955H1	1393	1484
4	208184.1	1500721T6	1405	1942
4	208184.1	2360410H1	1406	1679
4	208184.1	2360557H1	1406	1539
4	208184.1	g2023641	1411	1756
4	208184.1	2271884H1	1421	1705
4	208184.1	378111H1	1459	1630
4	208184.1	273132H1	1478	1606
4	208184.1	g4313046	1518	1980
4	208184.1	2130933H1	1526	1810
4	208184.1	2833701H1	990	1243
4	208184.1	1357760H1	994	1258
4	208184.1	4753736H1	1001	1285

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
4	208184.1	g4327798	1	405
4	208184.1	g3146292	2	336
4	208184.1	1837725H1	44	324
4	208184.1	g2466840	92	456
4	208184.1	467394H1	159	367
4	208184.1	2343544H1	267	506
4	208184.1	5942721H1	311	616
4	208184.1	2655870F6	521	1093
4	208184.1	1258044H1	521	758
4	208184.1	2655870H1	521	830
4	208184.1	1787374H1	560	844
4	208184.1	2479769H1	605	845
4	208184.1	3630251H1	607	894
4	208184.1	5589572H1	708	955
4	208184.1	2642468H1	777	1015
4	208184.1	2792888F6	782	1199
4	208184.1	3158506H1	869	1142
4	208184.1	830940H1	900	972
4	208184.1	2586835H1	928	1167
4	208184.1	3658943H1	938	1227
4	208184.1	647769H1	945	1164
4	208184.1	3330172H1	1542	1710
4	208184.1	g2968814	1552	1974
4	208184.1	3663020H1	1592	1883
4	208184.1	3662752H1	1593	1893
4	208184.1	1629365H1	1628	1855
4	208184.1	1629361H1	1628	1841
4	208184.1	393609F1	1631	1981
4	208184.1	393609R1	1631	1981
4	208184.1	g3145605	1636	1983
4	208184.1	g2318373	1640	1978
4	208184.1	2986775H1	1697	1990
4	208184.1	473722H1	1701	1933
4	208184.1	g2941595	1703	2001
4	208184.1	888824H1	1706	1955
4	208184.1	4132772H2	1734	1979
4	208184.1	g1378655	1744	1991
4	208184.1	g3174115	1744	2011
4	208184.1	g4327773	1775	1985
4	208184.1	g783328	1798	1975
4	208184.1	g1444361	1802	1975
4	208184.1	2352377H1	1802	1985
4	208184.1	g3837531	1924	1990
4	208184.1	700181H1	1378	1668
4	208184.1	2154043H1	1242	1524
4	208184.1	1500721H1	1248	1431
4	208184.1	1500721F6	1257	1748
4	208184.1	g1378654	1267	1587
4	208184.1	3051269H1	1274	1560
4	208184.1	g1296126	1279	1723

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
4	208184.1	g842860	1356	1604
4	208184.1	3727934T1	1363	1936
4	208184.1	2792888T6	1362	1938
4	208184.1	2655870T6	1366	1922
4	208184.1	642967R1	1368	1913
4	208184.1	642967H1	1369	1601
4	208184.1	645668H1	1369	1615
4	208184.1	869325R1	1143	1734
4	208184.1	734414R1	1172	1674
4	208184.1	734414H1	1172	1393
4	208184.1	515633H1	1009	1322
4	208184.1	g783327	1028	1265
4	208184.1	3167476H1	1039	1316
4	208184.1	2726328H1	1048	1300
4	208184.1	3578247H1	1055	1320
4	208184.1	1330851H1	1055	1296
4	208184.1	g1939112	1082	1314
4	208184.1	g1939111	1082	1322
4	208184.1	5426183H1	1105	1366
4	208184.1	1740885H1	1106	1341
4	208184.1	3727934H1	1117	1417
4	208184.1	869325H1	1143	1415
5	212029.3	1908946F6	1264	1619
5	212029.3	1908946H1	1264	1511
5	212029.3	g1958480	1322	1542
5	212029.3	2270984R6	1388	1847
5	212029.3	2270975H1	1388	1625
5	212029.3	2270984H1	1388	1617
5	212029.3	g850966	1509	1772
5	212029.3	987831H1	1587	1785
5	212029.3	g2069455	1	405
5	212029.3	1597036H1	1	218
5	212029.3	4013148H1	178	464
5	212029.3	g2064597	257	606
5	212029.3	3296932H1	313	565
5	212029.3	3296932F6	313	956
5	212029.3	5839392H1	316	547
5	212029.3	1254055H1	422	641
5	212029.3	3527901H1	436	710
5	212029.3	3402996H1	551	701
5	212029.3	3503954F6	617	1009
5	212029.3	3503954H1	618	921
5	212029.3	3985708H1	625	818
5	212029.3	3620240H1	773	982
5	212029.3	5912238H1	878	1073
5	212029.3	1961296H1	971	1244
5	212029.3	3406891F6	1033	1594
5	212029.3	3406891H1	1033	1273
5	212029.3	3296932T6	1256	1880
5	212029.3	4367370H2	1260	1508

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
6	213446.2	4544305H1	1	149
6	213446.2	5522542H1	30	291
6	213446.2	5522550H1	30	292
6	213446.2	1750451H1	95	304
6	213446.2	5328728H1	94	357
6	213446.2	1750451F6	94	648
6	213446.2	3359386H1	96	358
6	213446.2	796335R6	96	586
6	213446.2	3150909H1	97	331
6	213446.2	796335R1	96	644
6	213446.2	796335H1	96	329
6	213446.2	5424323H1	98	249
6	213446.2	3057114H1	96	297
6	213446.2	4673642H1	99	375
6	213446.2	4675219H1	99	220
6	213446.2	4673443H1	99	230
6	213446.2	603462H1	103	357
6	213446.2	603462R1	103	712
6	213446.2	4890190H1	144	432
6	213446.2	3456603H1	394	643
6	213446.2	5159788H1	438	661
6	213446.2	5096622H2	502	780
6	213446.2	3369950H1	627	914
6	213446.2	1487733H1	632	923
6	213446.2	g2321939	697	1107
6	213446.2	g4080503	832	1304
6	213446.2	5182853F6	856	1172
6	213446.2	5182853H1	856	1015
6	213446.2	5182853T6	859	1342
6	213446.2	g2656754	949	1317
6	213446.2	890504H1	1069	1263
6	213446.2	g4123800	1095	1321
7	228864.4	5865075H1	109	391
7	228864.4	1616880H1	109	333
7	228864.4	g774507	118	458
7	228864.4	4155366H1	120	391
7	228864.4	2362950H1	120	282
7	228864.4	2106089H1	120	368
7	228864.4	2362976H1	120	279
7	228864.4	1444952H1	120	400
7	228864.4	5697362H1	123	391
7	228864.4	g830103	122	525
7	228864.4	2503761H1	145	416
7	228864.4	3796285H1	145	479
7	228864.4	3079081H1	147	235
7	228864.4	869160H1	159	421
7	228864.4	869160R1	159	796
7	228864.4	3183023H1	177	496
7	228864.4	4560714H1	198	479
7	228864.4	1258418H1	207	449

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
7	228864.4	g389913	216	646
7	228864.4	3770688H1	222	367
7	228864.4	2533191H2	240	481
7	228864.4	3930940H1	268	571
7	228864.4	3537668H1	329	559
7	228864.4	2442003H1	330	520
7	228864.4	1319657H1	347	595
7	228864.4	2629730H1	357	612
7	228864.4	3481103H1	371	651
7	228864.4	3497710H1	384	685
7	228864.4	1873990H1	390	677
7	228864.4	5161918H1	404	682
7	228864.4	5263240H1	407	478
7	228864.4	2308843H1	419	526
7	228864.4	2743121H1	419	684
7	228864.4	3080645H1	426	726
7	228864.4	g1991438	427	704
7	228864.4	g1990985	427	788
7	228864.4	4078219H1	429	727
7	228864.4	5386816H1	433	716
7	228864.4	g613059	433	723
7	228864.4	1616645H1	435	683
7	228864.4	1616645F6	435	949
7	228864.4	g879155	457	630
7	228864.4	g907965	457	745
7	228864.4	698631H1	460	709
7	228864.4	495118H1	468	730
7	228864.4	495134H1	468	729
7	228864.4	1514782H1	485	705
7	228864.4	3296938H1	490	750
7	228864.4	4352776H1	494	706
7	228864.4	3480107H1	507	765
7	228864.4	1290794F6	517	877
7	228864.4	1290794H1	517	772
7	228864.4	4588579H1	521	805
7	228864.4	3107341H1	540	847
7	228864.4	4606551H1	541	812
7	228864.4	1463995H1	562	787
7	228864.4	g844939	592	867
7	228864.4	4752023H1	600	885
7	228864.4	2422049H1	603	836
7	228864.4	2620147H1	606	877
7	228864.4	739668H1	620	758
7	228864.4	1522232H1	618	812
7	228864.4	1519746H1	618	785
7	228864.4	739668R1	629	1119
7	228864.4	2309713H1	630	883
7	228864.4	3146554H1	640	978
7	228864.4	878372H1	643	912
7	228864.4	3457194H1	649	909

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
7	228864.4	3782086H1	661	989
7	228864.4	4567913H1	670	958
7	228864.4	1363758F1	670	1143
7	228864.4	4125731H1	670	950
7	228864.4	1363758H1	670	863
7	228864.4	1357005H1	670	951
7	228864.4	4045988H1	675	963
7	228864.4	g1886674	675	1127
7	228864.4	4775601H1	688	975
7	228864.4	5900350H1	717	870
7	228864.4	472426H1	734	904
7	228864.4	g2206480	738	912
7	228864.4	3153075H1	741	1034
7	228864.4	5841024H2	745	1038
7	228864.4	4574294H1	751	1023
7	228864.4	3784538H1	783	1107
7	228864.4	g1694080	789	1126
7	228864.4	4308240H1	788	1140
7	228864.4	3406691H1	789	1052
7	228864.4	3409828H1	803	1086
7	228864.4	g2032612	810	1160
7	228864.4	4255552H1	824	1104
7	228864.4	2956312H1	852	1180
7	228864.4	4379248H1	851	1140
7	228864.4	4378894H1	851	1027
7	228864.4	2411619H1	856	1103
7	228864.4	3504691H1	860	1153
7	228864.4	2642410H1	863	1121
7	228864.4	623141H1	868	1139
7	228864.4	2592655H1	867	1119
7	228864.4	4194450H1	867	1041
7	228864.4	2225947H1	867	1111
7	228864.4	g1186186	872	1088
7	228864.4	g1799037	874	1310
7	228864.4	1596221H1	874	1112
7	228864.4	4567877H1	878	1047
7	228864.4	2920003H1	876	1165
7	228864.4	2655503H1	880	1209
7	228864.4	264850H1	881	981
7	228864.4	6023806H1	883	1224
7	228864.4	1986159H1	883	1134
7	228864.4	1986159R6	883	1119
7	228864.4	2416335H1	883	1134
7	228864.4	3824142H1	894	1186
7	228864.4	5206556H1	895	1099
7	228864.4	4625676H1	901	1185
7	228864.4	171937H1	907	1124
7	228864.4	g888919	907	1190
7	228864.4	677587H1	918	1200
7	228864.4	2290038H1	919	1198

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
7	228864.4	5023768H1	928	1238
7	228864.4	g2001495	928	1282
7	228864.4	5183168H1	937	1205
7	228864.4	5879286H1	945	1240
7	228864.4	4184443H1	945	1150
7	228864.4	4211129H1	944	1240
7	228864.4	3272214H1	968	1249
7	228864.4	2572116H1	981	1288
7	228864.4	5112704H1	985	1308
7	228864.4	1911846H1	1003	1113
7	228864.4	g3307374	1444	1932
7	228864.4	g4111085	1450	1961
7	228864.4	1368277H1	1454	1710
7	228864.4	5261924H1	1459	1712
7	228864.4	536879H1	1462	1752
7	228864.4	1959881T6	1458	1920
7	228864.4	g2038223	1460	1768
7	228864.4	670986H1	1460	1801
7	228864.4	2372786H1	1460	1722
7	228864.4	1477817H1	1467	1738
7	228864.4	503758H1	1467	1751
7	228864.4	g2139339	1472	1967
7	228864.4	2415457H1	1478	1767
7	228864.4	g3429630	1483	1963
7	228864.4	1991354H1	1487	1804
7	228864.4	2508710H1	1499	1787
7	228864.4	g3087298	1500	1968
7	228864.4	g2354234	1502	1961
7	228864.4	g3250205	1507	1973
7	228864.4	g2264116	1507	1932
7	228864.4	g3245152	1514	1970
7	228864.4	g2526470	1515	1961
7	228864.4	g1860066	1517	1958
7	228864.4	1906229H1	1520	1845
7	228864.4	g2210895	1521	1947
7	228864.4	g3593403	1521	1970
7	228864.4	3107177H1	1526	1866
7	228864.4	5978491H1	1529	1857
7	228864.4	3350739H1	1534	1854
7	228864.4	1341266H1	1534	1843
7	228864.4	g2205403	1535	1974
7	228864.4	516461H1	1537	1798
7	228864.4	4253927H1	1544	1841
7	228864.4	g2805846	1543	1963
7	228864.4	2413301H1	1543	1800
7	228864.4	g2206749	1545	1964
7	228864.4	g2881920	1553	1967
7	228864.4	g3765236	1555	1972
7	228864.4	g1693975	1561	1962
7	228864.4	g1692741	1561	1973

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
7	228864.4	g3422186	1562	1968
7	228864.4	g2206375	1569	1961
7	228864.4	g2238997	1571	1984
7	228864.4	g2269218	1571	1961
7	228864.4	g1422987	1574	1958
7	228864.4	1366917H1	1576	1829
7	228864.4	1366917R1	1576	1937
7	228864.4	1366917T1	1576	1930
7	228864.4	g4509876	1576	1961
7	228864.4	g2840643	1576	1969
7	228864.4	873275T1	1577	1923
7	228864.4	873275H1	1577	1857
7	228864.4	873275R1	1577	1961
7	228864.4	943941H1	1582	1944
7	228864.4	943941T1	1581	1923
7	228864.4	553126H1	1590	1847
7	228864.4	g2955909	1587	1969
7	228864.4	g2141313	1592	1961
7	228864.4	841913H1	1595	1876
7	228864.4	1269237H1	1601	1895
7	228864.4	2240562H1	1600	1899
7	228864.4	1269229F6	1601	1961
7	228864.4	3173222H1	1601	1891
7	228864.4	1269229T6	1604	1921
7	228864.4	2569601H1	1605	1887
7	228864.4	008331H1	1607	1912
7	228864.4	g2410907	1607	1967
7	228864.4	g3870805	1607	1962
7	228864.4	g830045	1616	1978
7	228864.4	g4110296	1612	1976
7	228864.4	4595257H1	1618	1841
7	228864.4	g825912	1622	1973
7	228864.4	g1164606	1632	1961
7	228864.4	751050H1	1637	1898
7	228864.4	g1479705	1638	1961
7	228864.4	1257103F1	1642	1967
7	228864.4	1257103H1	1642	1924
7	228864.4	g519500	1644	1967
7	228864.4	2915847H1	1642	1944
7	228864.4	5427111H1	1646	1939
7	228864.4	210895H1	1646	1898
7	228864.4	g3050237	1647	1967
7	228864.4	2491624H1	1650	1906
7	228864.4	g3754764	1654	1966
7	228864.4	g858236	1661	1945
7	228864.4	g888828	1663	1967
7	228864.4	g832518	1669	1974
7	228864.4	3793365H1	1666	1961
7	228864.4	4424104H1	1670	1953
7	228864.4	g907936	1673	1946

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
7	228864.4	g2264098	1673	1933
7	228864.4	g2167663	1673	1966
7	228864.4	g1886251	1684	1964
7	228864.4	g3750664	1690	1961
7	228864.4	g1443124	1693	1967
7	228864.4	g889394	1695	1979
7	228864.4	g519496	1697	1967
7	228864.4	g614232	1699	1967
7	228864.4	2101758H1	1700	1967
7	228864.4	g994586	1701	1957
7	228864.4	g845833	1701	1967
7	228864.4	g810610	1701	1960
7	228864.4	g1067419	1701	1943
7	228864.4	1215929H1	1703	1857
7	228864.4	g872749	1706	1976
7	228864.4	g614200	1706	1961
7	228864.4	g566599	1710	1967
7	228864.4	g888655	1712	1968
7	228864.4	4425257H1	1715	1980
7	228864.4	240542H1	1716	1869
7	228864.4	g2058861	1715	1967
7	228864.4	g2335948	1720	1961
7	228864.4	g2322019	1726	1966
7	228864.4	530442H1	1741	1961
7	228864.4	g670640	1752	1967
7	228864.4	2245477H1	1755	1961
7	228864.4	5580560H1	1766	1929
7	228864.4	g1494073	1764	1961
7	228864.4	4194132H1	1766	1967
7	228864.4	g2986422	1785	1967
7	228864.4	g4123826	1797	1963
7	228864.4	1397558H1	1808	1961
7	228864.4	g1479653	1806	1961
7	228864.4	2258238H1	1808	1961
7	228864.4	1370863H1	1809	1967
7	228864.4	g2280375	1810	1967
7	228864.4	g916819	1817	1961
7	228864.4	g2739855	1840	1965
7	228864.4	g3038015	1842	1961
7	228864.4	g2841777	1852	1961
7	228864.4	g4372871	1855	1963
7	228864.4	1264942H1	1007	1273
7	228864.4	1264942R1	1007	1444
7	228864.4	405391R6	1014	1553
7	228864.4	5683210H1	1021	1289
7	228864.4	3541340H1	1019	1330
7	228864.4	215013H1	1035	1158
7	228864.4	g1928459	1047	1478
7	228864.4	1228283H1	1058	1320
7	228864.4	531728R6	1066	1706

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
7	228864.4	531728H1	1066	1371
7	228864.4	4092970H1	1066	1375
7	228864.4	5693116H1	1066	1331
7	228864.4	g614233	1077	1412
7	228864.4	5101746H1	1084	1332
7	228864.4	4642390H1	1105	1337
7	228864.4	866916H1	1109	1379
7	228864.4	866916R1	1109	1766
7	228864.4	1693363H1	1110	1207
7	228864.4	g810713	1114	1454
7	228864.4	g845887	1115	1544
7	228864.4	2214177H1	1118	1388
7	228864.4	1365249H1	1118	1190
7	228864.4	3853462H1	1118	1440
7	228864.4	g1940874	1119	1688
7	228864.4	3493702H1	1124	1439
7	228864.4	5004632H1	1128	1400
7	228864.4	3992620H1	1132	1456
7	228864.4	2874610H1	1130	1466
7	228864.4	1340384H1	1134	1308
7	228864.4	5184044H1	1142	1429
7	228864.4	5107670H1	1141	1413
7	228864.4	4425962H1	1142	1416
7	228864.4	2246674H1	1144	1434
7	228864.4	g2139112	1154	1646
7	228864.4	3663704H1	1155	1493
7	228864.4	2079688H1	1154	1447
7	228864.4	3591083H1	1154	1346
7	228864.4	3814383H1	1155	1476
7	228864.4	1681877H1	1154	1412
7	228864.4	2108278H1	1154	1458
7	228864.4	515405H1	1155	1403
7	228864.4	g858032	1157	1435
7	228864.4	1789187H1	1164	1422
7	228864.4	1788136H1	1164	1450
7	228864.4	4327161H1	1164	1437
7	228864.4	5832891H1	1184	1490
7	228864.4	276693H1	1181	1469
7	228864.4	g1521765	1194	1542
7	228864.4	5404066H1	1195	1483
7	228864.4	5404004H1	1195	1317
7	228864.4	1394880H1	1199	1488
7	228864.4	g922893	1204	1539
7	228864.4	g889937	1204	1539
7	228864.4	g889393	1205	1573
7	228864.4	g888654	1205	1448
7	228864.4	1917625H1	1209	1482
7	228864.4	2630585H1	1211	1488
7	228864.4	133967H1	1218	1422
7	228864.4	1616645T6	1227	1921

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
7	228864.4	g884600	1235	1593
7	228864.4	5840548H2	1241	1529
7	228864.4	4311468H1	1244	1447
7	228864.4	631129H1	1244	1534
7	228864.4	2130838H1	1244	1531
7	228864.4	g1692842	1243	1822
7	228864.4	752046R1	1254	1877
7	228864.4	2659504H1	1254	1562
7	228864.4	g1954716	1264	1577
7	228864.4	1538114H1	1268	1454
7	228864.4	4852290H1	1279	1549
7	228864.4	1950908H1	1283	1565
7	228864.4	112889H1	1293	1544
7	228864.4	2707203H1	1297	1577
7	228864.4	4317110H1	1298	1622
7	228864.4	531728T6	1302	1923
7	228864.4	405391T6	1302	1921
7	228864.4	112890H1	1306	1522
7	228864.4	g1961047	1306	1789
7	228864.4	6209217H1	1307	1670
7	228864.4	5106358H1	1308	1596
7	228864.4	198615916	1309	1922
7	228864.4	204430H1	1315	1474
7	228864.4	2220564H1	1317	1590
7	228864.4	g1973608	1327	1661
7	228864.4	5100480H1	1337	1447
7	228864.4	1886806H1	1340	1662
7	228864.4	g1576711	1341	1526
7	228864.4	g2069223	1343	1823
7	228864.4	137261H1	1343	1539
7	228864.4	g1423026	1343	1774
7	228864.4	604541H1	1343	1604
7	228864.4	3469340H1	1343	1631
7	228864.4	2438735H1	1351	1605
7	228864.4	g2069954	1351	1817
7	228864.4	2438390H1	1351	1627
7	228864.4	3126373H1	1354	1711
7	228864.4	2422970H1	1361	1653
7	228864.4	g2206156	1360	1739
7	228864.4	2316643H1	1370	1667
7	228864.4	2373160H1	1386	1695
7	228864.4	2364835H1	1386	1645
7	228864.4	1290794T6	1389	1952
7	228864.4	137894H1	1392	1604
7	228864.4	2627275H1	1392	1716
7	228864.4	4839445H1	1392	1726
7	228864.4	g2930378	1395	1970
7	228864.4	739668F1	1400	1961
7	228864.4	3251281H1	1399	1792
7	228864.4	2666633H1	1404	1692

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
7	228864.4	5834458H1	1409	1606
7	228864.4	3692921H1	1412	1754
7	228864.4	g2360187	1411	1932
7	228864.4	g2953905	1412	1964
7	228864.4	1489882H1	1415	1731
7	228864.4	3269028H1	1419	1599
7	228864.4	g1960172	1419	1961
7	228864.4	1346630H1	1419	1703
7	228864.4	g2051175	1421	1872
7	228864.4	2561963H1	1422	1759
7	228864.4	566676H1	1426	1766
7	228864.4	g2728469	1424	1970
7	228864.4	g3162592	1421	1945
7	228864.4	4536759H1	1427	1718
7	228864.4	g3665710	1430	1965
7	228864.4	1453494H1	1432	1717
7	228864.4	g3162610	1435	1945
7	228864.4	g4313225	1442	1951
7	228864.4	g4328835	1440	1970
7	228864.4	g888982	1882	1968
7	228864.4	1443349F6	1	514
7	228864.4	1739557H1	55	293
7	228864.4	3541425H1	63	374
7	228864.4	1594648H1	65	293
7	228864.4	868282H1	70	328
7	228864.4	4693320H2	76	177
7	228864.4	2437341H1	76	316
7	228864.4	1258508H1	79	348
7	228864.4	g677259	79	344
7	228864.4	2661646H1	82	327
7	228864.4	1992251H1	83	309
7	228864.4	2502018H1	83	356
7	228864.4	3700420H1	85	398
7	228864.4	1578634H1	87	320
7	228864.4	3601285H1	91	398
7	228864.4	3419979H1	91	366
7	228864.4	3394860H1	91	384
7	228864.4	3487463H1	91	397
7	228864.4	3323182H1	90	377
7	228864.4	3761644H1	92	455
7	228864.4	2190393H1	90	370
7	228864.4	2477729H1	91	320
7	228864.4	2925245H1	91	358
7	228864.4	3394839H1	91	359
7	228864.4	3394843H1	91	359
7	228864.4	660322H1	91	377
7	228864.4	2380023H1	91	329
7	228864.4	1687157H1	91	302
7	228864.4	3452490H1	91	264
7	228864.4	1959881H1	91	343

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
7	228864.4	660994H1	91	375
7	228864.4	2663372H1	91	340
7	228864.4	3496054H1	91	407
7	228864.4	1749148H1	91	374
7	228864.4	2797721H1	91	351
7	228864.4	2370507H1	91	388
7	228864.4	g872854	87	439
7	228864.4	3251075H1	91	419
7	228864.4	1959881R6	91	406
7	228864.4	3359733H1	92	390
7	228864.4	3557086H1	93	408
7	228864.4	2660652H1	95	349
7	228864.4	1875407H1	95	381
7	228864.4	5778376H1	98	388
7	228864.4	4839236H1	96	410
7	228864.4	4873821H1	97	392
7	228864.4	2267072H1	98	373
7	228864.4	4563807H1	102	187
7	228864.4	4697375H1	101	328
7	228864.4	g574327	101	473
7	228864.4	2457949H1	101	355
7	228864.4	g1959304	101	454
7	228864.4	4399256H1	101	258
7	228864.4	2525904H1	102	376
7	228864.4	750617H1	102	347
7	228864.4	4873985H1	102	367
7	228864.4	3296104H1	102	376
7	228864.4	2963248H1	101	426
7	228864.4	750617R1	102	654
7	228864.4	g826028	103	438
7	228864.4	4753330H1	104	385
7	228864.4	3466388H1	104	374
7	228864.4	3372760H1	104	385
7	228864.4	g831794	103	419
7	228864.4	3581563H1	105	406
7	228864.4	835615H1	105	348
7	228864.4	3239308H1	105	373
7	228864.4	732724R1	106	721
7	228864.4	732724H1	106	348
7	228864.4	3248690H1	106	424
7	228864.4	5919227H1	104	432
7	228864.4	5985820H1	108	389
8	229840.3	g3921683	2848	3070
8	229840.3	g2985904	2858	3072
8	229840.3	5909792H1	2693	2987
8	229840.3	g4189001	2712	3069
8	229840.3	g2882752	2717	3065
8	229840.3	g4073312	2728	3073
8	229840.3	g4264530	2733	3065
8	229840.3	g4325751	2738	3069

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
8	229840.3	g1148915	2739	3065
8	229840.3	g3836479	2744	3073
8	229840.3	1454580T6	2838	3037
8	229840.3	1454581H1	2838	3066
8	229840.3	1454581F1	2838	3065
8	229840.3	1454581T6	2838	3040
8	229840.3	g2782503	2842	3069
8	229840.3	3034701H1	2838	3063
8	229840.3	3000391H1	1647	1951
8	229840.3	5375263H1	1665	1869
8	229840.3	5375650H1	1665	1924
8	229840.3	4140779H1	1675	1982
8	229840.3	2880845T6	1739	2019
8	229840.3	785393H1	1796	2090
8	229840.3	1664014H1	1827	2057
8	229840.3	g3807773	1832	2305
8	229840.3	3323431H1	1888	2170
8	229840.3	4852173H1	3	263
8	229840.3	1573212T6	1903	2287
8	229840.3	4549830H1	1993	2265
8	229840.3	4995409H1	1944	2202
8	229840.3	2747040H1	1964	2208
8	229840.3	3878345H1	2032	2327
8	229840.3	3413323H1	2042	2290
8	229840.3	040203H1	2070	2308
8	229840.3	g3094583	456	932
8	229840.3	g3869975	473	933
8	229840.3	1348988T6	502	887
8	229840.3	g2398144	503	931
8	229840.3	g4069464	504	929
8	229840.3	3001122T6	565	905
8	229840.3	3001122H1	572	876
8	229840.3	3001122F6	573	932
8	229840.3	g3213774	588	935
8	229840.3	g2210579	662	941
8	229840.3	g4190109	681	929
8	229840.3	3002524H1	692	886
8	229840.3	5637815H1	748	1014
8	229840.3	g4327917	751	892
8	229840.3	3605342H1	760	1069
8	229840.3	1573212H1	872	1111
8	229840.3	1573212F6	872	1159
8	229840.3	5867496H1	913	1192
8	229840.3	5525935H2	972	1224
8	229840.3	5525917H2	972	1200
8	229840.3	g2210630	52	237
8	229840.3	2882517H1	55	320
8	229840.3	1348984H1	132	393
8	229840.3	1348988F6	132	569
8	229840.3	2303457T6	338	895

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
8	229840.3	2525337T6	394	899
8	229840.3	2548038T6	414	900
8	229840.3	4776015H1	16	291
8	229840.3	384074H1	22	310
8	229840.3	3201803H1	23	230
8	229840.3	2587779H1	34	280
8	229840.3	4358685H1	34	317
8	229840.3	4308601H1	34	325
8	229840.3	4308648H1	35	383
8	229840.3	426170H1	43	265
8	229840.3	828194H1	2400	2661
8	229840.3	1383318T6	2407	3027
8	229840.3	1487404H1	2412	2666
8	229840.3	878542R1	2428	3032
8	229840.3	878542H1	2428	2664
8	229840.3	878542T1	2428	3027
8	229840.3	2255908H1	2449	2735
8	229840.3	042254H1	2495	2695
8	229840.3	1676510H1	1463	1673
8	229840.3	3351180H1	1474	1763
8	229840.3	3164210H1	1482	1773
8	229840.3	6024893H1	1487	1789
8	229840.3	3294678H1	1513	1799
8	229840.3	3555380H1	1517	1822
8	229840.3	4370762H1	1551	1815
8	229840.3	3561882H1	1559	1860
8	229840.3	1664014T6	1570	2019
8	229840.3	2664716H1	1598	1827
8	229840.3	g2553076	1599	2055
8	229840.3	1664014F6	1603	2057
8	229840.3	g843066	1608	1908
8	229840.3	2811115H1	1619	1892
8	229840.3	1383318F6	1630	2128
8	229840.3	1383318H1	1630	1873
8	229840.3	939387H1	2858	3065
8	229840.3	960688H1	2858	2999
8	229840.3	g1784633	2858	3069
8	229840.3	g2987896	2858	3072
8	229840.3	4549830T1	2858	3026
8	229840.3	g3096610	2858	3069
8	229840.3	g1761395	2866	3042
8	229840.3	902367H1	2878	3064
8	229840.3	902367T1	2878	3036
8	229840.3	1370625H1	2883	3063
8	229840.3	1752509H1	2545	2763
8	229840.3	2174569T6	2550	3027
8	229840.3	3720838H1	2568	2887
8	229840.3	5680448H1	2580	2815
8	229840.3	g4189079	2584	3067
8	229840.3	g3927421	2595	3065

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
8	229840.3	1903055H1	2609	2815
8	229840.3	g3679709	2616	3074
8	229840.3	2133162H1	2660	2931
8	229840.3	779163H1	2685	2941
8	229840.3	4354675H1	2686	2815
8	229840.3	g2264632	2495	2815
8	229840.3	g2267837	2496	2838
8	229840.3	275005H1	2497	2653
8	229840.3	5076984H1	2508	2801
8	229840.3	1829765H1	2508	2744
8	229840.3	5076985H1	2509	2801
8	229840.3	1829765F6	2508	3038
8	229840.3	3995183H1	2514	2782
8	229840.3	182976576	2530	3023
8	229840.3	3519322H1	2082	2459
8	229840.3	2635539H1	2092	2363
8	229840.3	085879H1	2097	2364
8	229840.3	4852717H1	2096	2355
8	229840.3	3201459H1	2118	2314
8	229840.3	4980057H1	2124	2385
8	229840.3	g1785255	2144	2573
8	229840.3	3491811H1	2154	2423
8	229840.3	2471395H1	2215	2437
8	229840.3	3162006H1	2226	2511
8	229840.3	4996246H1	2229	2504
8	229840.3	g1761571	2288	2651
8	229840.3	2694820H1	2308	2482
8	229840.3	2622173H1	2326	2606
8	229840.3	g1925233	2364	2594
8	229840.3	828194T1	2400	3030
8	229840.3	828194R1	2400	2953
8	229840.3	g2540041	2946	3067
8	229840.3	g2539934	2959	3067
8	229840.3	g3055680	2978	3070
8	229840.3	2349363H1	2980	3069
8	229840.3	g1925117	2981	3066
8	229840.3	2880845F6	1118	1558
8	229840.3	2880845H1	1118	1415
8	229840.3	2174569F6	1251	1727
8	229840.3	2174569H1	1251	1475
8	229840.3	4872808H1	1284	1561
8	229840.3	838790H1	1299	1568
8	229840.3	2845321H1	1333	1592
8	229840.3	3389695H1	1346	1632
8	229840.3	2267707H1	1380	1630
8	229840.3	1549249H1	1442	1632
8	229840.3	3749030H1	1	191
8	229840.3	2548038F6	10	548
8	229840.3	2539058F6	10	624
8	229840.3	4561642H1	10	264

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
8	229840.3	2548038H1	10	261
8	229840.3	2303457H1	14	267
8	229840.3	2303457R6	14	487
8	229840.3	3714222H1	17	314
9	231793.2	3743582H1	1	301
9	231793.2	3490362H1	3	201
9	231793.2	3355002H1	21	304
9	231793.2	1522723H1	22	218
9	231793.2	2790244H2	30	337
9	231793.2	1866779F6	33	415
9	231793.2	1866779H1	33	315
9	231793.2	1311083H1	81	300
9	231793.2	3236153H1	112	360
9	231793.2	5158979H1	204	429
9	231793.2	1390212H1	289	447
9	231793.2	1390306H1	289	541
9	231793.2	1001126R6	326	885
9	231793.2	4049712H1	369	641
9	231793.2	3767101H1	536	651
9	231793.2	2791795H1	512	801
9	231793.2	4576054H1	565	824
9	231793.2	5593839H1	735	994
9	231793.2	5052279H1	837	971
9	231793.2	1986603R6	867	1390
9	231793.2	1986603H1	867	1148
9	231793.2	1991005H1	919	1076
9	231793.2	3962341H1	972	1262
9	231793.2	3673817H1	1007	1289
9	231793.2	2488457H1	1180	1409
9	231793.2	2623858H1	1187	1437
9	231793.2	2623858R6	1187	1501
9	231793.2	4650753H1	1351	1495
9	231793.2	2793766H1	1368	1667
9	231793.2	1803565H1	1553	1837
9	231793.2	5281570H2	1575	1847
9	231793.2	4731704H1	1578	1869
9	231793.2	158289H1	1659	1835
9	231793.2	4048712H1	1710	1992
9	231793.2	1707686H1	1780	1971
9	231793.2	5296093H1	1783	2004
9	231793.2	g1979679	1792	2097
9	231793.2	g2277027	1844	2232
9	231793.2	2673033F6	1878	2419
9	231793.2	2673033H1	1878	2118
9	231793.2	977810H1	1886	2105
9	231793.2	5027277H1	1892	2169
9	231793.2	3803405H1	1935	2246
9	231793.2	5095560H1	1943	2126
9	231793.2	4213438H1	1971	2181
9	231793.2	1986603T6	1984	2479

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
9	231793.2	1001126T6	1992	2477
9	231793.2	1803565T6	2006	2466
9	231793.2	4170673H1	2050	2319
9	231793.2	3406618H1	2052	2313
9	231793.2	1866779T7	2068	2484
9	231793.2	g3765637	2072	2541
9	231793.2	5094942H1	2071	2324
9	231793.2	1214293T6	2088	2483
9	231793.2	1214293R6	2089	2496
9	231793.2	1214293H1	2099	2319
9	231793.2	1214167H1	2100	2353
9	231793.2	g2347914	2126	2520
9	231793.2	5084768H1	2127	2351
9	231793.2	1914969H1	2130	2392
9	231793.2	g3049752	2143	2523
9	231793.2	1707686T6	2151	2476
9	231793.2	5048501H1	2163	2459
9	231793.2	2673033T6	2179	2484
9	231793.2	g2556740	2194	2521
9	231793.2	g4078219	2241	2545
9	231793.2	2883970T6	2276	2504
9	231793.2	3512992H1	2276	2482
9	231793.2	g2322181	2353	2523
9	231793.2	1302067T7	2358	2481
9	231793.2	1302517H1	2365	2521
9	231793.2	1302517F6	2365	2521
9	231793.2	134723H1	2380	2521
9	231793.2	g1195715	2479	2529
10	234137.5	1832689R6	409	751
10	234137.5	1711521H1	413	622
10	234137.5	3317846H1	475	733
10	234137.5	g1616066	508	785
10	234137.5	2185641H1	526	792
10	234137.5	1618067H1	569	786
10	234137.5	1255603F6	593	951
10	234137.5	1255603H1	593	840
10	234137.5	5518712H1	592	827
10	234137.5	1944240H1	206	468
10	234137.5	g814646	194	490
10	234137.5	3746685H1	207	493
10	234137.5	2486355H1	212	459
10	234137.5	2888507H1	194	257
10	234137.5	2500535H1	212	454
10	234137.5	3511080H1	198	505
10	234137.5	2503636H1	258	508
10	234137.5	698952H1	275	372
10	234137.5	699726H1	275	547
10	234137.5	699737H1	275	542
10	234137.5	5190833H2	287	547
10	234137.5	2723787H1	285	555

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
10	234137.5	4880881H1	289	506
10	234137.5	1742695H1	1192	1399
10	234137.5	g1004759	1193	1454
10	234137.5	3051736H1	1198	1493
10	234137.5	3789688H1	1215	1430
10	234137.5	389357H1	1221	1370
10	234137.5	4000387H1	1237	1509
10	234137.5	535718H1	1253	1466
10	234137.5	454365R1	1440	1754
10	234137.5	2419654H1	316	571
10	234137.5	1993760H1	317	548
10	234137.5	3506477H1	317	624
10	234137.5	g991858	324	495
10	234137.5	g4152671	380	748
10	234137.5	3327435H1	381	647
10	234137.5	1832689H1	409	689
10	234137.5	2110777R6	1	348
10	234137.5	2110777H1	1	190
10	234137.5	714010H1	26	224
10	234137.5	g706051	26	417
10	234137.5	g674497	27	384
10	234137.5	6026756H1	34	308
10	234137.5	3530615H1	141	458
10	234137.5	4171108H1	155-	454
10	234137.5	g615415	154	412
10	234137.5	3156905H1	161	328
10	234137.5	g1815065	164	624
10	234137.5	g884950	168	595
10	234137.5	3331405H1	173	444
10	234137.5	3458347H1	183	429
10	234137.5	3672287H1	177	400
10	234137.5	2816025H1	181	495
10	234137.5	4077622H1	178	467
10	234137.5	905762H1	180	395
10	234137.5	g953765	180	561
10	234137.5	1602692H1	183	396
10	234137.5	1602692F6	183	487
10	234137.5	g775373	184	485
10	234137.5	1482169H1	182	462
10	234137.5	g2141035	183	625
10	234137.5	4159960H1	186	452
10	234137.5	g616022	185	466
10	234137.5	g705506	186	492
10	234137.5	g705505	186	460
10	234137.5	g868789	190	488
10	234137.5	g831177	190	564
10	234137.5	g574383	189	529
10	234137.5	g1516946	192	619
10	234137.5	g390441	190	506
10	234137.5	3243071H1	194	448

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
10	234137.5	2888320H1	194	481
10	234137.5	2180954H1	778	935
10	234137.5	901500R1	614	1145
10	234137.5	4230253H1	1101	1384
10	234137.5	901600H1	614	922
10	234137.5	589607H1	1148	1398
10	234137.5	901500H1	614	907
10	234137.5	901744H1	614	815
10	234137.5	2287212H1	1189	1422
10	234137.5	5591962H1	633	765
10	234137.5	3424013H1	1190	1460
10	234137.5	1742570H1	1192	1478
10	234137.5	g4394560	1660	2001
10	234137.5	g4224234	1598	2008
11	234671.14	4638731H1	73	352
11	234671.14	2525135H1	71	327
11	234671.14	4510615H1	90	235
11	234671.14	2805957H1	91	423
11	234671.14	5912661H1	90	401
11	234671.14	2016655H1	93	419
11	234671.14	3202510H1	95	401
11	234671.14	4608993H1	95	350
11	234671.14	725606H1	95	408
11	234671.14	5030359H1	94	349
11	234671.14	1499350H1	95	308
11	234671.14	4849095H2	101	299
11	234671.14	2916364H1	100	405
11	234671.14	2071479H1	100	380
11	234671.14	4294695H1	105	191
11	234671.14	1480701H1	100	313
11	234671.14	2845388H1	103	388
11	234671.14	3916903H1	104	433
11	234671.14	4974316H1	104	402
11	234671.14	2865203H1	104	214
11	234671.14	916311H1	105	433
11	234671.14	915496H1	105	392
11	234671.14	2220048T6	106	668
11	234671.14	g1799327	103	346
11	234671.14	g735496	108	456
11	234671.14	2521203H1	108	377
11	234671.14	2820807H1	109	330
11	234671.14	5302702H1	111	380
11	234671.14	2367817H1	115	386
11	234671.14	2660131H1	116	374
11	234671.14	g1962046	115	562
11	234671.14	2220048F6	118	622
11	234671.14	5622009H1	115	475
11	234671.14	088730H1	119	393
11	234671.14	g2036474	120	433
11	234671.14	3978238H1	121	442

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
11	234671.14	4744991H1	121	397
11	234671.14	3529614H1	122	458
11	234671.14	g1697240	122	306
11	234671.14	g1721900	122	613
11	234671.14	3928785H1	122	406
11	234671.14	4626904H1	122	396
11	234671.14	3928677H1	122	305
11	234671.14	g1516296	122	603
11	234671.14	2074823H1	122	270
11	234671.14	2135894H1	122	418
11	234671.14	3115158H1	123	430
11	234671.14	2135876H1	122	420
11	234671.14	575915H1	126	291
11	234671.14	4975637H1	126	419
11	234671.14	1463657H1	131	349
11	234671.14	g1317142	132	626
11	234671.14	1463657T1	131	669
11	234671.14	5278514H1	131	296
11	234671.14	1914942H1	132	399
11	234671.14	2479730H1	132	391
11	234671.14	3148758H1	132	461
11	234671.14	2912447H1	132	425
11	234671.14	5857652H1	134	429
11	234671.14	2451454H1	134	392
11	234671.14	5664881H1	135	444
11	234671.14	4981466H1	136	420
11	234671.14	2968710H1	136	486
11	234671.14	4981166H1	136	419
11	234671.14	3013140H1	136	389
11	234671.14	2551737H1	136	422
11	234671.14	2284544H1	136	397
11	234671.14	102120H1	136	407
11	234671.14	3461073H1	136	399
11	234671.14	4822658H1	139	441
11	234671.14	4166805H1	136	467
11	234671.14	2707011H1	137	428
11	234671.14	4974307H1	139	436
11	234671.14	1468622H1	139	275
11	234671.14	1467020H1	139	345
11	234671.14	2541676H1	139	415
11	234671.14	1470317H1	139	341
11	234671.14	3733432H1	141	464
11	234671.14	g901576	143	487
11	234671.14	2766646H1	143	411
11	234671.14	082496H1	149	367
11	234671.14	2476615H1	148	390
11	234671.14	2905015H1	149	325
11	234671.14	3760125H1	156	272
11	234671.14	3297065H1	160	435
11	234671.14	6141029H1	159	505

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
11	234671.14	2818173H1	161	414
11	234671.14	4701519H1	163	457
11	234671.14	2371480H1	165	412
11	234671.14	2448051H1	165	429
11	234671.14	2026733H1	165	446
11	234671.14	086299H1	165	447
11	234671.14	4553646H1	167	446
11	234671.14	3236203H1	170	447
11	234671.14	2625102H1	170	425
11	234671.14	g1639954	171	396
11	234671.14	g1447865	190	407
11	234671.14	g889618	204	571
11	234671.14	3292442F6	1	493
11	234671.14	3292442H1	1	261
11	234671.14	2787149H1	22	144
11	234671.14	4845874H1	64	251
11	234671.14	5217923H1	69	348
11	234671.14	3292442T6	204	689
11	234671.14	g889628	204	548
11	234671.14	5509259H1	218	458
11	234671.14	3035317H1	223	544
11	234671.14	3035317F6	223	561
11	234671.14	g4329558	240	715
11	234671.14	g4111623	244	720
11	234671.14	g3404679	245	707
11	234671.14	g4112201	246	707
11	234671.14	g2929715	248	707
11	234671.14	g3401096	253	710
11	234671.14	4206791H1	273	465
11	234671.14	g2268964	287	706
11	234671.14	419449H1	292	516
11	234671.14	2763433T6	293	678
11	234671.14	g1516236	295	718
11	234671.14	1999242H1	310	512
11	234671.14	g504586	313	710
11	234671.14	g1721788	314	716
11	234671.14	4372931H1	321	579
11	234671.14	1353392F1	323	760
11	234671.14	1353392H1	323	599
11	234671.14	g3797245	334	707
11	234671.14	g1728570	340	716
11	234671.14	4711787H1	383	484
11	234671.14	g735497	401	718
11	234671.14	2534033H1	406	647
11	234671.14	347531H1	412	659
11	234671.14	498396H1	419	637
11	234671.14	g2327885	426	722
11	234671.14	g3048289	426	915
11	234671.14	g3756898	428	714
11	234671.14	5408101H1	428	529

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
11	234671.14	g3202140	430	720
11	234671.14	g2875495	436	750
11	234671.14	g4194406	439	715
11	234671.14	g3600863	461	915
11	234671.14	548974H1	498	715
11	234671.14	g3180704	511	572
11	234671.14	001841H1	517	911
11	234671.14	g2904348	534	918
11	234671.14	g1300605	535	712
11	234671.14	g3843537	558	920
11	234671.14	g2716778	564	715
11	234671.14	4704563H1	567	707
11	234671.14	5094769H1	613	856
11	234671.14	g1147845	641	923
11	234671.14	3774346H1	676	970
11	234671.14	3237695H1	694	853
11	234671.14	3549570H1	731	986
11	234671.14	1306053F6	737	1223
11	234671.14	6104976H1	853	1149
11	234671.14	534062H1	914	1164
11	234671.14	2673834H1	931	1145
11	234671.14	g4292281	998	1448
11	234671.14	1306053H1	994	1223
11	234671.14	g3803923	1028	1448
11	234671.14	g2768559	1065	1453
11	234671.14	g3415483	1115	1459
11	234671.14	659821R6	1144	1458
11	234671.14	659821T6	1143	1410
11	234671.14	659821H1	1144	1407
11	234671.14	g3659045	1159	1406
11	234671.14	g2344002	1193	1447
11	234671.14	g889629	1209	1385
11	234671.14	g889619	1254	1401
11	234671.14	g901577	1258	1448
11	234671.14	g908490	1258	1402
11	234671.14	2374770H1	1344	1458
12	241236.3	g4083561	1571	2017
12	241236.3	2491474H1	1570	1818
12	241236.3	g4222338	1572	2016
12	241236.3	4883514T6	1574	1994
12	241236.3	g4082140	1581	1953
12	241236.3	2129206H1	1590	1898
12	241236.3	g2177776	1593	2016
12	241236.3	g4077506	1605	2010
12	241236.3	1456253R1	1613	2014
12	241236.3	2752225H1	1623	1900
12	241236.3	g4189365	1624	2019
12	241236.3	g3144764	1626	2014
12	241236.3	g2539525	1650	2013
12	241236.3	g2986682	1666	2017

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
12	241236.3	g2273603	1701	2012
12	241236.3	2989623T6	1740	1966
12	241236.3	2625824H1	1750	1989
12	241236.3	2625824T6	1758	1956
12	241236.3	2625824F6	1750	2010
12	241236.3	g3756824	1	393
12	241236.3	5376769H1	1	249
12	241236.3	3473825H1	115	374
12	241236.3	1675287H1	134	303
12	241236.3	1675845H1	135	314
12	241236.3	2047281F6	271	810
12	241236.3	2047281H1	271	482
12	241236.3	3724339H1	352	632
12	241236.3	5733241H1	404	664
12	241236.3	4909488H1	408	664
12	241236.3	1857844H1	412	667
12	241236.3	3078885H1	467	776
12	241236.3	4883514F6	529	963
12	241236.3	4883514H1	529	815
12	241236.3	g1023658	566	798
12	241236.3	1222879H1	644	871
12	241236.3	3400427H1	661	890
12	241236.3	1702383H1	664	880
12	241236.3	4902281H1	687	953
12	241236.3	4380777H1	697	956
12	241236.3	868686H1	702	954
12	241236.3	2598561H1	706	994
12	241236.3	3672519H1	718	995
12	241236.3	5811931H1	729	1048
12	241236.3	4863967H1	769	1059
12	241236.3	1534650H1	780	979
12	241236.3	4852733H1	780	1034
12	241236.3	1532438H1	780	987
12	241236.3	3407892H1	791	1049
12	241236.3	4173535H1	841	1129
12	241236.3	736762H1	845	1073
12	241236.3	987503H1	867	1107
12	241236.3	3591339H1	899	1203
12	241236.3	1600224H1	907	1096
12	241236.3	1680682H1	924	1117
12	241236.3	984876R1	967	1431
12	241236.3	5022045H1	967	1235
12	241236.3	984876H1	967	1272
12	241236.3	2394790H1	995	1238
12	241236.3	3105586H1	1029	1318
12	241236.3	2116090H1	1029	1295
12	241236.3	g3894545	1045	1441
12	241236.3	1665126H1	1048	1280
12	241236.3	2812429H1	1096	1416
12	241236.3	3099677H1	1102	1419

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
12	241236.3	3323472H1	1109	1397
12	241236.3	3806144H1	1111	1421
12	241236.3	1967610H1	1112	1402
12	241236.3	2967854H1	1112	1426
12	241236.3	g1627157	1114	1405
12	241236.3	3812578H1	1117	1273
12	241236.3	2808537H1	1122	1393
12	241236.3	2265394H1	1125	1400
12	241236.3	5573683H1	1130	1367
12	241236.3	603729H1	1139	1413
12	241236.3	2594490H1	1151	1408
12	241236.3	2083413H1	1153	1440
12	241236.3	606483H1	1210	1377
12	241236.3	336504H1	1227	1467
12	241236.3	g1114699	1226	1411
12	241236.3	4903237H1	1276	1552
12	241236.3	1976619F6	1276	1737
12	241236.3	1976619H1	1276	1544
12	241236.3	1738833H1	1299	1487
12	241236.3	1738865F6	1299	1601
12	241236.3	4240709H1	1343	1407
12	241236.3	4240711H1	1343	1709
12	241236.3	g853461	1360	1657
12	241236.3	2123125H1	1368	1658
12	241236.3	5451102H1	1372	1637
12	241236.3	2191211H1	1382	1653
12	241236.3	g1792059	1408	1780
12	241236.3	543835H1	1412	1649
12	241236.3	1977130T6	1425	1965
12	241236.3	1633344H1	1427	1669
12	241236.3	4505552H1	1428	1707
12	241236.3	1976619T6	1433	1970
12	241236.3	5022045T1	1438	1972
12	241236.3	1738865T6	1441	1967
12	241236.3	1981924H1	1459	1759
12	241236.3	2803121H1	1495	1769
12	241236.3	2260917H1	1503	1771
12	241236.3	3014105H1	1509	1829
12	241236.3	1994356H1	1513	1799
12	241236.3	5568339H1	1525	1765
12	241236.3	3186679H1	1537	1873
12	241236.3	4828122H1	1544	1837
12	241236.3	4828623H1	1544	1807
12	241236.3	g3595120	1549	2018
12	241236.3	g2177775	1559	2016
12	241236.3	1456253H1	1562	1841
12	241236.3	1000028H1	1564	1808
12	241236.3	3791315H1	1567	1881
12	241236.3	g4392232	1568	2013
12	241236.3	g2968124	1767	2016

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
12	241236.3	4115186H1	1773	2017
12	241236.3	3392646H1	1783	2058
12	241236.3	g3239075	1838	2014
12	241236.3	g3808002	1848	2016
12	241236.3	g4072387	1848	2014
12	241236.3	3781961H1	1848	2169
12	241236.3	g3754629	1851	2016
12	241236.3	g4006032	1860	2015
12	241236.3	g4073569	1860	2010
12	241236.3	g4005900	1870	2007
12	241236.3	g3321490	1862	2009
12	241236.3	g4006303	1870	2007
12	241236.3	g4087154	1871	2010
12	241236.3	g3862359	1871	2010
12	241236.3	g3322077	1862	2015
12	241236.3	g4005537	1871	2010
12	241236.3	g3846653	1871	2010
12	241236.3	g4077466	1862	2010
12	241236.3	g4080249	1871	2011
12	241236.3	g3862436	1871	2010
12	241236.3	g4018950	1863	2007
12	241236.3	g4077665	1871	2010
12	241236.3	g3989227	1871	2010
12	241236.3	g3806894	1864	2014
12	241236.3	g3932638	1871	2011
12	241236.3	g3862447	1871	2010
12	241236.3	g3847853	1871	2010
12	241236.3	g3989984	1871	2010
12	241236.3	g3890144	1871	2011
12	241236.3	g3989001	1871	2010
12	241236.3	g4071839	1871	2008
12	241236.3	g3847054	1871	2008
12	241236.3	g3989318	1871	2016
12	241236.3	g3890413	1871	2016
12	241236.3	g3848056	1871	2007
12	241236.3	g4282452	1871	2007
12	241236.3	g4018579	1871	2014
12	241236.3	g3990148	1871	2014
12	241236.3	g3890229	1871	2010
12	241236.3	g3847713	1871	2010
12	241236.3	504961H1	1872	2018
12	241236.3	2475277H1	1872	2017
12	241236.3	g3149294	1964	2016
13	245014.1	168004H1	1773	2112
13	245014.1	168004R6	1777	2032
13	245014.1	3444984H1	1854	2115
13	245014.1	963645H1	1859	2101
13	245014.1	963645R2	1859	2354
13	245014.1	g3095484	1869	1985
13	245014.1	2278942H1	1903	2171

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
13	245014.1	3993577H1	1907	2200
13	245014.1	3518094H1	1918	2179
13	245014.1	5696350H1	1918	2173
13	245014.1	4507976H1	1924	2192
13	245014.1	3020932H1	1924	2204
13	245014.1	4400157H1	1949	2191
13	245014.1	3248110H1	1949	2229
13	245014.1	2855006H1	1949	2041
13	245014.1	5399133H1	1	213
13	245014.1	3450361R6	68	543
13	245014.1	3450361H1	68	327
13	245014.1	2731452F6	81	421
13	245014.1	2731452H1	81	320
13	245014.1	263691H1	94	428
13	245014.1	5674201H1	106	347
13	245014.1	2645021H1	207	460
13	245014.1	g895569	346	512
13	245014.1	1923470T6	2455	2704
13	245014.1	1923470R6	2469	2742
13	245014.1	1923470H1	2469	2740
13	245014.1	g1874511	2471	2748
13	245014.1	g3179513	2407	2746
13	245014.1	g1153232	2416	2748
13	245014.1	2285748H1	2426	2679
13	245014.1	2875652H1	2477	2743
13	245014.1	g878521	2504	2740
13	245014.1	g2810267	2508	2751
13	245014.1	g4457618	2512	2745
13	245014.1	1860061T6	2430	2701
13	245014.1	1636359H1	2527	2620
13	245014.1	974331H1	2439	2619
13	245014.1	g1548974	2445	2740
13	245014.1	4802874H1	2527	2633
13	245014.1	2785026H1	2528	2716
13	245014.1	g2209561	2448	2743
13	245014.1	2862743H1	2558	2742
13	245014.1	g2208300	2452	2740
13	245014.1	g2987537	2624	2751
13	245014.1	3318766H1	1684	1957
13	245014.1	4825016H1	1699	1982
13	245014.1	3776745H1	1732	2032
13	245014.1	4368674H1	1746	2008
13	245014.1	2650579H1	1749	1945
13	245014.1	5062862H1	1764	2021
13	245014.1	5062961H2	1766	2004
13	245014.1	4089945H1	1770	1847
13	245014.1	2631802T6	2246	2706
13	245014.1	4863733H1	2264	2562
13	245014.1	5328806H1	2261	2544
13	245014.1	g3917411	2269	2748

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
13	245014.1	g2838934	2255	2747
13	245014.1	3166548H1	2273	2559
13	245014.1	g2818702	2280	2690
13	245014.1	g3693781	2261	2742
13	245014.1	g1068825	2306	2659
13	245014.1	g3016160	2306	2749
13	245014.1	607473H1	2309	2584
13	245014.1	3558364H1	2329	2637
13	245014.1	g4329144	2346	2738
13	245014.1	g1941347	2347	2733
13	245014.1	4302681H1	2356	2591
13	245014.1	g3182104	2369	2745
13	245014.1	1299474T6	2371	2705
13	245014.1	1299474F6	2377	2742
13	245014.1	g2003283	2377	2742
13	245014.1	1302005H1	2380	2722
13	245014.1	g1219422	2396	2743
13	245014.1	178082H1	1590	1829
13	245014.1	064892H1	1591	1750
13	245014.1	963385H1	1595	1896
13	245014.1	963385R2	1595	1972
13	245014.1	g1068873	1463	1775
13	245014.1	2280635H1	1470	1750
13	245014.1	145623R1	1453	1886
13	245014.1	960167H1	1546	1671
13	245014.1	g1166309	1456	1851
13	245014.1	3638263H1	1553	1845
13	245014.1	5423560H1	1615	1861
13	245014.1	1495185H1	1633	1857
13	245014.1	g2209742	1636	2103
13	245014.1	927457H1	1650	1930
13	245014.1	722266H1	1650	1917
13	245014.1	929020H1	1650	1913
13	245014.1	927457R1	1650	2180
13	245014.1	g1874627	1666	1896
13	245014.1	g1920695	1632	1830
13	245014.1	637604H1	1672	1906
13	245014.1	g1958169	1678	1988
13	245014.1	g959179	1452	1761
13	245014.1	3038691H1	1453	1545
13	245014.1	3398816H1	1453	1567
13	245014.1	4212104H1	937	1209
13	245014.1	5500792H1	976	1201
13	245014.1	6012320H1	996	1270
13	245014.1	2675268H1	1000	1244
13	245014.1	2675268F6	1000	1405
13	245014.1	3724087H1	1035	1309
13	245014.1	3069566H1	1096	1395
13	245014.1	5508358H1	1126	1346
13	245014.1	5592345H1	1278	1487

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
13	245014.1	141058H1	1278	1534
13	245014.1	3714983H1	1373	1661
13	245014.1	3515644H1	1417	1647
13	245014.1	4797535H1	360	650
13	245014.1	g1128352	373	613
13	245014.1	g2003284	456	712
13	245014.1	4164512H1	367	675
13	245014.1	g878573	547	871
13	245014.1	2749018H1	576	825
13	245014.1	345036116	593	1156
13	245014.1	2910268H1	610	873
13	245014.1	4372565H1	613	915
13	245014.1	133005H1	618	801
13	245014.1	133005R6	618	1056
13	245014.1	4972429H1	693	985
13	245014.1	4435621H1	735	1012
13	245014.1	g3446618	746	1207
13	245014.1	3275925H1	745	986
13	245014.1	5299476H1	746	899
13	245014.1	g2541414	754	1204
13	245014.1	3629224H1	1987	2293
13	245014.1	160092H1	2017	2421
13	245014.1	3256601H1	2029	2284
13	245014.1	5091829H1	1988	2256
13	245014.1	3489772H1	2057	2357
13	245014.1	g2057259	2087	2423
13	245014.1	g395755	2096	2414
13	245014.1	218809H1	2112	2381
13	245014.1	3493510H1	2011	2285
13	245014.1	217964H1	2112	2345
13	245014.1	1376993F1	2115	2581
13	245014.1	1376993H1	2115	2356
13	245014.1	113469H1	2014	2268
13	245014.1	1860061F6	2124	2549
13	245014.1	1860061H1	2124	2428
13	245014.1	3806342H1	2014	2255
13	245014.1	828638H1	2137	2406
13	245014.1	828638R1	2137	2607
13	245014.1	5710216H2	2171	2422
13	245014.1	344609H1	2015	2226
13	245014.1	4121876H1	2174	2394
13	245014.1	4416742H1	2176	2434
13	245014.1	133005T6	2176	2707
13	245014.1	145623F1	2183	2740
13	245014.1	5500510H1	2192	2451
13	245014.1	g2444538	2195	2559
13	245014.1	g2163904	2198	2658
13	245014.1	004038H1	2203	2582
13	245014.1	003770H1	2203	2566
13	245014.1	003808H1	2203	2532

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
13	245014.1	4356958H1	2221	2498
13	245014.1	168004T6	2222	2703
13	245014.1	3858354H1	2235	2426
13	245014.1	3858174H1	2236	2531
13	245014.1	4602871H1	768	1018
13	245014.1	2884645H1	776	1041
13	245014.1	4196193H1	873	1007
13	245014.1	g2139409	887	1282
13	245014.1	2872604H1	890	1150
13	245014.1	4548678H1	890	1121
13	245014.1	g1953042	915	1165
13	245014.1	3438285H1	1440	1656
13	245014.1	2462626H1	1448	1680
13	245014.1	3491523H1	1440	1685
14	245251.6	g3806445	1422	1590
14	245251.6	g3806467	1422	1590
14	245251.6	g3848606	1422	1590
14	245251.6	g3849478	1422	1590
14	245251.6	g3845826	1422	1590
14	245251.6	g3806471	1422	1590
14	245251.6	g3846603	1422	1590
14	245251.6	g4034496	1422	1594
14	245251.6	g3807003	1422	1591
14	245251.6	g3806382	1422	1593
14	245251.6	g3847027	1422	1587
14	245251.6	g3989330	1422	1587
14	245251.6	g3861794	1422	1587
14	245251.6	g4018012	1422	1593
14	245251.6	g3847094	1422	1591
14	245251.6	g3807437	1422	1593
14	245251.6	g3846856	1422	1592
14	245251.6	g4284777	1422	1586
14	245251.6	g3847587	1422	1593
14	245251.6	g4186360	1422	1593
14	245251.6	g3990433	1422	1593
14	245251.6	g3807539	1422	1593
14	245251.6	g3990700	1422	1593
14	245251.6	g4071417	1422	1593
14	245251.6	g3806276	1422	1592
14	245251.6	g3806906	1422	1592
14	245251.6	g3847511	1422	1592
14	245251.6	g3842268	1422	1593
14	245251.6	g3846164	1422	1592
14	245251.6	g3846151	1422	1592
14	245251.6	g4077836	1422	1594
14	245251.6	g3862401	1422	1593
14	245251.6	g4082235	1422	1593
14	245251.6	g3847852	1422	1593
14	245251.6	g3842306	1422	1591
14	245251.6	g4074675	1422	1591

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
14	245251.6	g3861509	1422	1593
14	245251.6	g3989299	1422	1593
14	245251.6	g4074633	1422	1591
14	245251.6	g3848075	1422	1593
14	245251.6	g3847601	1422	1596
14	245251.6	g3846659	1422	1591
14	245251.6	g3807971	1422	1593
14	245251.6	g3862373	1422	1592
14	245251.6	g3846613	1422	1594
14	245251.6	g3842371	1422	1593
14	245251.6	g4150319	1422	1593
14	245251.6	g3848195	1422	1593
14	245251.6	g4186335	1422	1593
14	245251.6	g4071420	1422	1590
14	245251.6	g3845843	1422	1590
14	245251.6	271945H1	1423	1592
14	245251.6	4860092H1	1425	1549
14	245251.6	3025205H1	1425	1591
14	245251.6	g1329015	1110	1592
14	245251.6	1708907H1	1110	1392
14	245251.6	2356035H1	1113	1395
14	245251.6	g3321637	1412	1593
14	245251.6	g3321397	1412	1591
14	245251.6	g3990361	1412	1594
14	245251.6	g3321297	1412	1594
14	245251.6	g3321613	1412	1590
14	245251.6	g3321619	1412	1590
14	245251.6	g3321346	1412	1590
14	245251.6	g3321642	1412	1592
14	245251.6	g3322073	1412	1593
14	245251.6	g3322037	1412	1579
14	245251.6	g3321904	1412	1591
14	245251.6	g3322057	1412	1594
14	245251.6	g4086504	1412	1593
14	245251.6	g3321689	1412	1593
14	245251.6	g3322072	1412	1594
14	245251.6	290509H1	1413	1593
14	245251.6	g3842429	1413	1595
14	245251.6	g3321374	1416	1590
14	245251.6	2715779H1	1417	1590
14	245251.6	g3841465	1420	1590
14	245251.6	g3847930	1421	1590
14	245251.6	g3847580	1421	1592
14	245251.6	g4187012	1421	1590
14	245251.6	g3806657	1421	1586
14	245251.6	g3846129	1421	1590
14	245251.6	g4005749	1421	1592
14	245251.6	g4005487	1421	1590
14	245251.6	g3665836	1422	1590
14	245251.6	g3848560	1422	1590

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
14	245251.6	g3845838	1422	1590
14	245251.6	g3848559	1422	1590
14	245251.6	703105H1	1113	1417
14	245251.6	g1501582	1117	1592
14	245251.6	g3255080	1119	1602
14	245251.6	g4081903	1119	1598
14	245251.6	g1948394	1156	1590
14	245251.6	2411955H1	1117	1414
14	245251.6	4569146H1	1120	1459
14	245251.6	027069H1	1165	1412
14	245251.6	1538171H1	1120	1407
14	245251.6	g3279555	1127	1593
14	245251.6	g4114349	1128	1594
14	245251.6	g3740354	1131	1592
14	245251.6	g2279150	1132	1590
14	245251.6	g4533152	1132	1592
14	245251.6	g3962173	1132	1596
14	245251.6	887316H1	1138	1466
14	245251.6	g2397876	1165	1592
14	245251.6	g2360627	1138	1598
14	245251.6	g2714133	1137	1590
14	245251.6	g3016485	1165	1596
14	245251.6	g2464368	1139	1594
14	245251.6	g2552766	1146	1590
14	245251.6	2962133H1	1150	1496
14	245251.6	g2464621	1152	1589
14	245251.6	537878H1	1150	1446
14	245251.6	1359957H1	1148	1419
14	245251.6	1963987H1	1155	1496
14	245251.6	g3253832	1165	1593
14	245251.6	g2913751	1168	1593
14	245251.6	g2932949	1173	1602
14	245251.6	g3735276	1178	1602
14	245251.6	863137H1	1181	1466
14	245251.6	g4269459	1181	1590
14	245251.6	g2563609	1183	1590
14	245251.6	2418779H1	1185	1471
14	245251.6	g4113654	1188	1590
14	245251.6	g1641703	1188	1586
14	245251.6	1551309H1	1190	1448
14	245251.6	g3840122	1192	1597
14	245251.6	g2705424	1200	1589
14	245251.6	2286469H1	1200	1498
14	245251.6	g2566862	1209	1593
14	245251.6	g2435745	1212	1361
14	245251.6	2088012H1	1215	1517
14	245251.6	1312225H1	1215	1472
14	245251.6	g2270163	1215	1592
14	245251.6	2288870H1	1215	1497
14	245251.6	g864236	1220	1591

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
14	245251.6	g3597473	1220	1598
14	245251.6	g1972695	1223	1595
14	245251.6	g3322133	1231	1594
14	245251.6	g1148477	1231	1598
14	245251.6	g3960762	1244	1590
14	245251.6	272932H1	1248	1590
14	245251.6	3334564H1	1248	1581
14	245251.6	1355971H1	1248	1540
14	245251.6	1907330H1	1248	1548
14	245251.6	g1774782	1253	1594
14	245251.6	g927896	1244	1592
14	245251.6	g2279391	1256	1596
14	245251.6	g3280855	1259	1597
14	245251.6	981518H1	1265	1598
14	245251.6	g3070488	1267	1596
14	245251.6	g4269675	1271	1593
14	245251.6	g3127594	1273	1545
14	245251.6	g4297922	1273	1593
14	245251.6	g1527256	1274	1590
14	245251.6	g3215022	1273	1593
14	245251.6	g1927427	1278	1590
14	245251.6	g1618008	1279	1599
14	245251.6	g651970	1270	1597
14	245251.6	1926049H1	1279	1543
14	245251.6	g2053209	1281	1601
14	245251.6	770417H1	1425	1593
14	245251.6	g3321693	1426	1590
14	245251.6	544220H1	1464	1596
14	245251.6	g3886402	1465	1859
14	245251.6	422119H1	1493	1594
14	245251.6	4832225H1	721	877
14	245251.6	063120H1	727	876
14	245251.6	3228413H1	720	863
14	245251.6	g1927545	717	883
14	245251.6	1255835H1	754	894
14	245251.6	3226250H1	699	837
14	245251.6	4323801H1	746	909
14	245251.6	4510868H1	704	796
14	245251.6	4800865H1	700	891
14	245251.6	3715312H1	697	900
14	245251.6	1428725H1	696	883
14	245251.6	2106521H1	480	642
14	245251.6	5100266H1	695	785
14	245251.6	1222560H1	693	907
14	245251.6	360061H1	701	914
14	245251.6	2388047H1	692	901
14	245251.6	g1527303	817	919
14	245251.6	1708351H1	699	916
14	245251.6	4563631H1	839	920
14	245251.6	4337368H1	720	919

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
14	245251.6	3284155H1	811	915
14	245251.6	1573816H1	427	644
14	245251.6	g2017060	687	914
14	245251.6	g2992991	687	808
14	245251.6	5945233H1	692	816
14	245251.6	142800H1	686	921
14	245251.6	1611073H1	686	892
14	245251.6	1612960H1	686	871
14	245251.6	5182909H1	686	922
14	245251.6	4675087H1	686	868
14	245251.6	2175031H1	686	917
14	245251.6	1674874H1	686	901
14	245251.6	748598H1	699	925
14	245251.6	g698473	1	375
14	245251.6	g2750955	3	322
14	245251.6	4711779H1	41	296
14	245251.6	2468527H1	173	531
14	245251.6	3674073H1	243	527
14	245251.6	g2015374	251	676
14	245251.6	4710904H1	283	582
14	245251.6	3674243H1	289	527
14	245251.6	5112393H1	314	606
14	245251.6	1960508H1	317	627
14	245251.6	4043372H1	322	607
14	245251.6	2017147H1	341	444
14	245251.6	1725960H1	376	592
14	245251.6	1573484H1	377	596
14	245251.6	310542H1	382	643
14	245251.6	3205850H1	400	693
14	245251.6	1726232H1	403	592
14	245251.6	310938H1	407	646
14	245251.6	1877685H1	417	704
14	245251.6	2598596H1	416	704
14	245251.6	3090278H1	416	704
14	245251.6	4128553H1	426	699
14	245251.6	g2030260	426	715
14	245251.6	5538163H1	448	647
14	245251.6	2502707H1	450	699
14	245251.6	1800655H1	462	705
14	245251.6	4899818H1	465	705
14	245251.6	3858619H1	464	724
14	245251.6	2111517H1	478	729
14	245251.6	310488H1	476	642
14	245251.6	1686443H1	491	731
14	245251.6	1425427H1	584	837
14	245251.6	1490475H1	584	812
14	245251.6	4853210H1	586	806
14	245251.6	g3846065	1396	1590
14	245251.6	g4304887	1396	1593
14	245251.6	g4006580	1396	1590

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
14	245251.6	g4085914	1396	1590
14	245251.6	g4005760	1396	1592
14	245251.6	g3931547	1396	1593
14	245251.6	g3842208	1396	1590
14	245251.6	g4082237	1399	1590
14	245251.6	g3848014	1403	1590
14	245251.6	g3322137	1406	1590
14	245251.6	g3883898	1407	1587
14	245251.6	g4086951	1407	1590
14	245251.6	g4033921	1408	1590
14	245251.6	g4077315	1409	1590
14	245251.6	g3849422	1409	1587
14	245251.6	g3322163	1409	1590
14	245251.6	g4005466	1410	1596
14	245251.6	g4189675	1409	1587
14	245251.6	g3842222	1410	1593
14	245251.6	g4073579	1410	1593
14	245251.6	g4071991	1410	1593
14	245251.6	g3848782	1410	1590
14	245251.6	g3842461	1410	1590
14	245251.6	g3890086	1410	1589
14	245251.6	g4073751	1410	1587
14	245251.6	g4072155	1410	1587
14	245251.6	g4005762	1410	1587
14	245251.6	g4017767	1410	1586
14	245251.6	g4082225	1410	1633
14	245251.6	g4150699	1410	1587
14	245251.6	g3849075	1410	1590
14	245251.6	g3842220	1410	1590
14	245251.6	g4034488	1410	1592
14	245251.6	g4018592	1410	1590
14	245251.6	g4071488	1410	1590
14	245251.6	g3990408	1410	1584
14	245251.6	g4006140	1410	1587
14	245251.6	g4148813	1410	1592
14	245251.6	g3665905	1410	1591
14	245251.6	g4189666	1410	1586
14	245251.6	g3842450	1410	1590
14	245251.6	g4006752	1410	1593
14	245251.6	g3665891	1410	1595
14	245251.6	g3848888	1410	1590
14	245251.6	g4393782	1410	1590
14	245251.6	g3927687	1410	1594
14	245251.6	g3931504	1410	1589
14	245251.6	g3922922	1411	1589
14	245251.6	g3321965	1412	1590
14	245251.6	g3321608	1412	1591
14	245251.6	g3321192	1412	1590
14	245251.6	g3321212	1412	1593
14	245251.6	g3848884	1412	1631

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
14	245251.6	g3321780	1412	1590
14	245251.6	g3321859	1412	1590
14	245251.6	g3322187	1412	1596
14	245251.6	g3846123	1412	1587
14	245251.6	g3321441	1412	1590
14	245251.6	g3322011	1412	1591
14	245251.6	g3754224	1049	1606
14	245251.6	g3425292	1050	1595
14	245251.6	4996361H1	1014	1361
14	245251.6	4546463H1	1019	1337
14	245251.6	g3117255	1018	1545
14	245251.6	g2357822	1020	1592
14	245251.6	1853257H1	1021	1384
14	245251.6	g1722623	1022	1593
14	245251.6	g2566601	1026	1486
14	245251.6	g1328830	1031	1601
14	245251.6	g2824176	1029	1592
14	245251.6	g4124629	1041	1595
14	245251.6	g2269348	1044	1592
14	245251.6	g4217707	1045	1593
14	245251.6	g4070671	1048	1601
14	245251.6	2240628H1	1047	1379
14	245251.6	g4524298	3	185
14	245251.6	g4005797	8	142
14	245251.6	813528H1	686	905
14	245251.6	g3807474	1283	1416
14	245251.6	g4327570	1238	1419
14	245251.6	1645004H1	451	672
14	245251.6	1312584H1	697	963
14	245251.6	3471164H1	720	993
14	245251.6	4998559H1	722	1004
14	245251.6	g3890267	1283	1418
14	245251.6	4351329H1	686	824
14	245251.6	1672134H1	1233	1423
14	245251.6	g3848850	1283	1415
14	245251.6	1517530H1	462	672
14	245251.6	g2037443	332	608
14	245251.6	3315274H1	739	996
14	245251.6	g3990415	1283	1419
14	245251.6	g3849121	1283	1415
14	245251.6	3272177H1	680	917
14	245251.6	5913406H1	686	954
14	245251.6	g3848236	1283	1417
14	245251.6	052757H1	756	994
14	245251.6	4708284H1	686	930
14	245251.6	g3848935	1283	1416
14	245251.6	g3890340	8	142
14	245251.6	g2025954	684	995
14	245251.6	1990122H1	581	672
14	245251.6	1436841H1	686	906

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SEQ ID NO:	Template ID	Component ID	Start	Stop
14	245251.6	g1301526	726	979
14	245251.6	g3990448	1283	1417
14	245251.6	5902523H1	694	996
14	245251.6	2154086H1	740	1016
14	245251.6	917108H1	686	847
14	245251.6	2767517H1	686	922
14	245251.6	g3862612	1283	1419
14	245251.6	g3848684	6	142
14	245251.6	1814125H1	1258	1419
14	245251.6	3682120H1	697	991
14	245251.6	2053508H1	751	1005
14	245251.6	3291620H1	686	907
14	245251.6	g3862415	1283	1419
14	245251.6	545078H1	734	994
14	245251.6	3280782H1	759	1005
14	245251.6	5376980H1	475	673
14	245251.6	3749492H1	686	950
14	245251.6	g3847665	10	142
14	245251.6	1469717H1	864	1150
14	245251.6	2442618H1	869	1184
14	245251.6	5161050T6	873	1570
14	245251.6	2814583T6	874	1553
14	245251.6	5216384H1	888	1183
14	245251.6	g1313327	885	1234
14	245251.6	506895H1	887	1161
14	245251.6	2246148H1	888	1183
14	245251.6	g2032570	892	1215
14	245251.6	g2033061	892	1312
14	245251.6	6105423H1	892	1228
14	245251.6	1212338H1	894	1249
14	245251.6	2681270H1	894	1239
14	245251.6	2408072H1	894	1201
14	245251.6	774022H1	894	1152
14	245251.6	4667376H1	894	1218
14	245251.6	2629364H1	894	1225
14	245251.6	2260118H1	894	1198
14	245251.6	4372704H1	895	1264
14	245251.6	464993H1	896	1176
14	245251.6	3027714H1	896	1274
14	245251.6	1856953H1	911	1241
14	245251.6	2410246H1	911	1181
14	245251.6	4750638H2	911	1243
14	245251.6	1294624H1	913	1179
14	245251.6	738970H1	921	1241
14	245251.6	g1775058	924	1381
14	245251.6	g1618108	929	1261
14	245251.6	g2336997	938	1260
14	245251.6	1979648H1	940	1271
14	245251.6	1990936H1	941	1143
14	245251.6	966663H1	946	1300

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
14	245251.6	4371102H1	955	1331
14	245251.6	g1315094	957	1239
14	245251.6	4369280H1	963	1293
14	245251.6	1905865H1	993	1281
14	245251.6	g1972974	997	1364
14	245251.6	4068060H1	1006	1188
14	245251.6	g3597449	1007	1595
14	245251.6	1657456H1	1009	1264
14	245251.6	4996367H1	1014	1326
14	245251.6	g1758102	1094	1593
14	245251.6	g1623171	1100	1594
14	245251.6	g2824662	1099	1590
14	245251.6	g2526734	1101	1590
14	245251.6	g4108545	1103	1592
14	245251.6	g2328692	1105	1593
14	245251.6	814904H1	1104	1425
14	245251.6	2870889H1	1108	1460
14	245251.6	5295918H1	686	922
14	245251.6	g3890756	1283	1419
14	245251.6	3086975H1	686	955
14	245251.6	g3990539	1283	1416
14	245251.6	g3847105	1283	1417
14	245251.6	g3989389	6	142
14	245251.6	1333963H1	686	884
14	245251.6	g4077443	9	142
14	245251.6	3180014H1	686	913
14	245251.6	g3849458	8	142
14	245251.6	4619650H1	686	907
14	245251.6	g3989412	1283	1416
14	245251.6	491316H1	686	911
14	245251.6	g4077428	7	142
14	245251.6	1647829H1	686	881
14	245251.6	g3848848	1283	1416
14	245251.6	705929H1	686	889
14	245251.6	g3806474	1283	1418
14	245251.6	2540850H1	686	937
14	245251.6	2301130H1	715	965
14	245251.6	g3849235	1283	1411
14	245251.6	127489H1	686	893
14	245251.6	g3848866	1283	1419
14	245251.6	1876624H1	383	664
14	245251.6	g4085932	9	142
14	245251.6	g4077334	1283	1419
14	245251.6	g3890303	1283	1415
14	245251.6	3384767H1	725	969
14	245251.6	3688995H1	686	945
14	245251.6	1215027H1	839	975
14	245251.6	g3847032	1283	1416
14	245251.6	g3807516	8	142
14	245251.6	5102970H1	686	941

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
14	245251.6	1802892H1	736	973
14	245251.6	g3842338	7	142
14	245251.6	3286343H2	719	969
14	245251.6	1874116H1	374	653
14	245251.6	g3806912	1283	1416
14	245251.6	g3847485	6	142
14	245251.6	619293H1	687	930
14	245251.6	1258505H1	720	968
14	245251.6	g3989388	1283	1411
14	245251.6	6007911H1	686	974
14	245251.6	2149173H1	686	956
14	245251.6	g3848208	1283	1419
14	245251.6	2992493H1	686	946
14	245251.6	650586H1	379	638
14	245251.6	g3849247	1283	1416
14	245251.6	5910613H1	686	972
14	245251.6	g4077711	1283	1419
14	245251.6	4510726H1	704	973
14	245251.6	g3848062	1283	1417
14	245251.6	6106933H1	686	919
14	245251.6	5115225H1	697	970
14	245251.6	g3846901	6	142
14	245251.6	2513695H2	686	907
14	245251.6	g4326234	1283	1419
14	245251.6	3158887H1	686	935
14	245251.6	2706363H1	756	1102
14	245251.6	g4535116	756	1070
14	245251.6	3883004H1	760	1087
14	245251.6	5301496H1	760	1055
14	245251.6	4096707H1	760	1122
14	245251.6	2863619H1	763	1162
14	245251.6	2867319H1	763	1102
14	245251.6	g1281850	767	1331
14	245251.6	g1576704	773	1232
14	245251.6	g1298432	777	1130
14	245251.6	3837476H1	784	1091
14	245251.6	3010150H1	785	1128
14	245251.6	3010801H1	785	1123
14	245251.6	g2204501	790	1201
14	245251.6	g2217814	791	1325
14	245251.6	g1060431	795	1137
14	245251.6	3918458H1	803	1125
14	245251.6	5697844H1	803	1122
14	245251.6	g2591145	815	1249
14	245251.6	4573806H1	818	1102
14	245251.6	4914643H1	820	1142
14	245251.6	908962H1	833	1192
14	245251.6	213202276	833	1548
14	245251.6	4628839H1	832	1120
14	245251.6	3550659H1	835	1213

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
14	245251.6	g674861	839	1124
14	245251.6	706061H1	843	1165
14	245251.6	2061068H1	851	1161
14	245251.6	5264515F6	853	1331
14	245251.6	g2539208	854	1344
14	245251.6	2408850H1	856	1132
14	245251.6	6006938H1	863	1213
14	245251.6	6007037H1	863	1228
14	245251.6	3171466H1	866	1199
14	245251.6	g1124148	1283	1592
14	245251.6	g3803160	1285	1600
14	245251.6	g2942025	1286	1598
14	245251.6	3160175H1	1288	1592
14	245251.6	g1740568	1300	1593
14	245251.6	2300048H1	1302	1557
14	245251.6	g2877399	1307	1594
14	245251.6	g2728321	1309	1591
14	245251.6	1491834H1	1310	1593
14	245251.6	2862613H1	1317	1592
14	245251.6	945012H1	1322	1598
14	245251.6	g847168	1313	1593
14	245251.6	g4327571	1325	1590
14	245251.6	1507186H1	1330	1569
14	245251.6	3970589H1	1334	1595
14	245251.6	209179H1	1334	1535
14	245251.6	207014H1	1334	1582
14	245251.6	3967178H1	1335	1590
14	245251.6	g3058131	1337	1592
14	245251.6	3967462H1	1335	1591
14	245251.6	g2787682	1337	1594
14	245251.6	g3154417	1337	1594
14	245251.6	2361006H1	1338	1590
14	245251.6	2362930H1	1339	1590
14	245251.6	g3001273	1339	1590
14	245251.6	g3960768	1341	1592
14	245251.6	942262H1	1345	1592
14	245251.6	902954H1	1349	1593
14	245251.6	4506855H1	1353	1590
14	245251.6	g1265337	1360	1599
14	245251.6	1419110H1	1365	1590
14	245251.6	g1264701	1373	1599
14	245251.6	g1227017	1374	1600
14	245251.6	g3884934	1385	1589
14	245251.6	g3884396	1388	1590
14	245251.6	g3884926	1390	1587
14	245251.6	g3846626	1390	1593
14	245251.6	g3849105	1390	1541
14	245251.6	g3884831	1391	1593
14	245251.6	g3842214	1391	1590
14	245251.6	g3846730	1393	1590

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
14	245251.6	g3846909	1393	1586
14	245251.6	g2657904	1087	1590
14	245251.6	g4525345	1090	1592
14	245251.6	g3239030	1088	1599
14	245251.6	870032H1	1092	1407
14	245251.6	5597455H1	1093	1365
14	245251.6	1898558H1	697	967
14	245251.6	g4071850	1283	1419
14	245251.6	2452174H1	686	897
14	245251.6	2842830H1	380	650
14	245251.6	3686824H1	686	972
14	245251.6	g4077526	9	142
14	245251.6	3782176H1	686	945
14	245251.6	1535425H1	861	972
14	245251.6	g3848055	1283	1419
14	245251.6	3119950H1	699	977
14	245251.6	3884464H1	686	806
14	245251.6	g3842568	6	142
14	245251.6	3507042H1	695	977
14	245251.6	2512439H1	686	909
14	245251.6	g4085946	1283	1416
14	245251.6	4405615H1	686	943
14	245251.6	5896519H1	694	977
14	245251.6	g3845926	1283	1419
14	245251.6	3330695H1	686	929
14	245251.6	g3847726	1283	1416
14	245251.6	3157747H1	693	975
14	245251.6	1622382H1	686	909
14	245251.6	g3862513	1283	1419
14	245251.6	1656661H1	686	873
14	245251.6	g3845948	8	142
14	245251.6	3028871H1	686	967
14	245251.6	3809687H1	686	977
14	245251.6	g3990041	1283	1417
14	245251.6	2451959H1	573	669
14	245251.6	4551365H1	699	976
14	245251.6	g3847599	6	142
14	245251.6	5172386H1	721	980
14	245251.6	g3845822	1283	1416
14	245251.6	4824541H1	726	980
14	245251.6	g3931555	1283	1418
14	245251.6	g4006049	9	142
14	245251.6	2481849H1	686	907
14	245251.6	6026544H1	686	978
14	245251.6	g3862408	1283	1416
14	245251.6	5893562H1	694	984
14	245251.6	3141501H1	686	935
14	245251.6	g2899544	48	137
14	245251.6	g3842538	9	142
14	245251.6	1897745H1	686	935

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
14	245251.6	g3807515	10	142
14	245251.6	3698231H1	686	964
14	245251.6	1680096H1	454	670
14	245251.6	3575006H1	686	976
14	245251.6	3945268H1	696	980
14	245251.6	g3990060	1283	1418
14	245251.6	1630619H1	740	961
14	245251.6	6026541H1	686	983
14	245251.6	282261H1	821	987
14	245251.6	g3989332	1283	1416
14	245251.6	g2714757	6	127
14	245251.6	g3848017	1283	1418
14	245251.6	4909050H1	691	864
14	245251.6	g4077616	1283	1419
14	245251.6	5016694H1	709	985
14	245251.6	g2715675	1342	1421
14	245251.6	g3890469	1283	1415
14	245251.6	g2020485	727	976
14	245251.6	g1548162	1304	1422
14	245251.6	g4086845	1283	1419
14	245251.6	3095012H1	686	984
14	245251.6	g3990363	1283	1416
14	245251.6	4012002H1	686	964
14	245251.6	g2198225	1301	1421
14	245251.6	g3989049	10	142
14	245251.6	2960954H1	686	985
14	245251.6	g4189209	1283	1419
14	245251.6	4268413H1	686	983
14	245251.6	850512H1	756	961
14	245251.6	4238523H1	696	976
14	245251.6	g3989140	1283	1419
14	245251.6	g715951	690	981
14	245251.6	g3736535	1367	1423
14	245251.6	2512088H1	686	984
14	245251.6	g4284258	9	142
14	245251.6	4379339H1	686	936
14	245251.6	g3890461	1283	1419
14	245251.6	3182012H1	687	981
14	245251.6	4706886H1	686	932
14	245251.6	g3846611	1283	1415
14	245251.6	2322530H1	736	987
14	245251.6	g3990086	7	142
14	245251.6	3839096H1	686	938
14	245251.6	321302H1	765	984
14	245251.6	g3989015	1283	1416
14	245251.6	1990623H1	686	928
14	245251.6	3683615H1	696	987
14	245251.6	g4086491	1283	1416
14	245251.6	1619567H1	686	866
14	245251.6	3078410H1	686	986

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
14	245251.6	g4080312	9	142
14	245251.6	2908167H1	686	987
14	245251.6	3671767H1	686	892
14	245251.6	g2037878	686	961
14	245251.6	g4077435	1283	1416
14	245251.6	1603854H1	686	878
14	245251.6	g1199063	686	987
14	245251.6	g4017782	1283	1419
14	245251.6	1347327H1	686	907
14	245251.6	g927989	359	637
14	245251.6	3324035H1	697	990
14	245251.6	g4086445	7	142
14	245251.6	2546965H2	686	862
14	245251.6	4343132H1	873	997
14	245251.6	g4077453	1283	1419
14	245251.6	4334622H1	686	944
14	245251.6	g847231	356	637
14	245251.6	g3846130	1283	1416
14	245251.6	g4018630	1283	1416
14	245251.6	2101272H1	4	114
14	245251.6	2587234H1	686	903
14	245251.6	3574372H1	686	979
14	245251.6	g3694286	1050	1590
14	245251.6	g1315095	1061	1599
14	245251.6	210059H1	1053	1331
14	245251.6	g3279541	1055	1598
14	245251.6	g3736864	1055	1595
14	245251.6	4974349H1	1056	1417
14	245251.6	g3665039	1061	1592
14	245251.6	3888183H1	1063	1401
14	245251.6	1530540H1	1063	1345
14	245251.6	g1274050	1076	1590
14	245251.6	002239H1	1065	1548
14	245251.6	1297924H1	1065	1381
14	245251.6	3479370H1	1065	1328
14	245251.6	1312352H1	1068	1333
14	245251.6	506800H1	1068	1356
14	245251.6	g1364437	1077	1592
14	245251.6	g2214112	1072	1591
14	245251.6	1267456H1	1074	1366
14	245251.6	g2820951	1079	1594
14	245251.6	1311167H1	1082	1398
14	245251.6	g2401841	1080	1593
14	245251.6	g3735785	1082	1596
14	245251.6	g2217605	1083	1595
14	245251.6	g1576739	1085	1592
14	245251.6	g674787	1092	1587
14	245251.6	4010641H1	697	1030
14	245251.6	2506513H1	697	956
14	245251.6	795092H1	697	957

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SEQ ID NO:	Template ID	Component ID	Start	Stop
14	245251.6	5221852H2	697	979
14	245251.6	5687479H1	697	979
14	245251.6	1483887H1	697	973
14	245251.6	1449209H1	697	917
14	245251.6	3747027H1	697	1031
14	245251.6	1594015H1	697	942
14	245251.6	1455584H1	697	966
14	245251.6	1593886H1	697	922
14	245251.6	3379095H1	699	975
14	245251.6	526768H1	699	978
14	245251.6	g1970187	700	1120
14	245251.6	5913596H1	699	1013
14	245251.6	g1997336	702	1120
14	245251.6	g864282	704	1088
14	245251.6	4307655H1	702	1087
14	245251.6	3766134H1	702	1031
14	245251.6	4545031H1	705	1032
14	245251.6	g1501684	705	1219
14	245251.6	g1321292	707	1229
14	245251.6	2496344H1	705	1103
14	245251.6	4675111H1	705	964
14	245251.6	3482217H1	705	1067
14	245251.6	4070047H1	705	1031
14	245251.6	2997014H1	706	1031
14	245251.6	g1623223	711	1097
14	245251.6	5164521H1	709	999
14	245251.6	4196137H1	686	806
14	245251.6	358653H1	701	923
14	245251.6	1370775H1	686	823
14	245251.6	3759039H1	686	907
14	245251.6	600085H1	422	656
14	245251.6	1575013H1	686	897
14	245251.6	1000003H1	686	925
14	245251.6	2049730H1	686	925
14	245251.6	5282003H1	686	919
14	245251.6	5161050H1	557	657
14	245251.6	2134833H1	696	928
14	245251.6	4667193H1	689	928
14	245251.6	1593935H1	686	898
14	245251.6	1786467H1	686	919
14	245251.6	1299188H1	686	917
14	245251.6	2616796H1	686	913
14	245251.6	5699823H1	686	928
14	245251.6	4833390H1	691	907
14	245251.6	2450956H1	686	913
14	245251.6	1416169H1	686	927
14	245251.6	4902593H1	686	853
14	245251.6	685823H1	686	795
14	245251.6	1378622H1	686	892
14	245251.6	2203295H1	686	912

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SEQ ID NO:	Template ID	Component ID	Start	Stop
14	245251.6	4873526H1	686	906
14	245251.6	1567661H1	686	889
14	245251.6	4265241H1	554	660
14	245251.6	4565002H1	686	930
14	245251.6	5028562H1	686	931
14	245251.6	3315321H2	686	916
14	245251.6	179704H1	686	857
14	245251.6	5043044H1	691	923
14	245251.6	3272310H1	686	923
14	245251.6	5590795H1	686	871
14	245251.6	4374880H1	686	930
14	245251.6	2942376H1	722	932
14	245251.6	2669414H1	686	932
14	245251.6	2051081H1	686	932
14	245251.6	778957H1	686	836
14	245251.6	3383437H1	686	924
14	245251.6	2502860H1	702	939
14	245251.6	g1548213	686	828
14	245251.6	1558658H1	686	895
14	245251.6	2742568H1	693	934
14	245251.6	5844527H1	686	928
14	245251.6	3237925H1	413	660
14	245251.6	1654956H1	686	903
14	245251.6	1212747H1	686	906
14	245251.6	2110510H1	695	937
14	245251.6	2670483H1	697	937
14	245251.6	3887565H1	686	937
14	245251.6	2278236H1	692	939
14	245251.6	1549915H1	686	880
14	245251.6	1915263H1	686	926
14	245251.6	3174435H1	686	912
14	245251.6	931246H1	686	925
14	245251.6	1524019H1	724	944
14	245251.6	2630203H1	686	914
14	245251.6	6063419H1	686	867
14	245251.6	1557962H1	686	876
14	245251.6	1519653H1	686	820
14	245251.6	g1970343	686	927
14	245251.6	1643982H1	686	870
14	245251.6	2636948H1	686	944
14	245251.6	3236095H1	686	910
14	245251.6	3290990H1	695	944
14	245251.6	2916653H1	439	664
14	245251.6	2347442H1	686	901
14	245251.6	2160657H1	705	942
14	245251.6	1612904H1	686	861
14	245251.6	1602311H1	686	865
14	245251.6	2479177H1	686	940
14	245251.6	3276325H1	686	942
14	245251.6	3342181H1	686	942

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SEQ ID NO:	Template ID	Component ID	Start	Stop
14	245251.6	3414248H1	700	942
14	245251.6	4244690H1	424	664
14	245251.6	1657385H1	686	887
14	245251.6	2060168H1	686	942
14	245251.6	2724864H1	686	940
14	245251.6	2507348H1	718	943
14	245251.6	3439967H1	686	916
14	245251.6	3875717H1	712	946
14	245251.6	3930892H1	686	944
14	245251.6	2876429H1	686	930
14	245251.6	1663347H1	686	897
14	245251.6	745654H1	715	946
14	245251.6	5714032H1	402	661
14	245251.6	6013561H1	686	939
14	245251.6	3368428H1	687	945
14	245251.6	4673619H1	686	945
14	245251.6	4356555H1	686	921
14	245251.6	2984258H1	691	943
14	245251.6	6073987H1	686	945
14	245251.6	2435338H1	686	881
14	245251.6	3416993H1	698	943
14	245251.6	4108736H1	686	944
14	245251.6	1793902H1	686	938
14	245251.6	3429779H1	686	943
14	245251.6	1522075H1	468	664
14	245251.6	3282589H1	701	946
14	245251.6	5781877H1	686	925
14	245251.6	1311376H1	686	946
14	245251.6	2478308H1	686	912
14	245251.6	476523H1	1305	1419
14	245251.6	3406437H1	6	108
14	245251.6	4998161H1	686	936
14	245251.6	1759883H1	686	943
14	245251.6	2426656H1	686	918
14	245251.6	2357554H1	686	898
14	245251.6	911731H1	686	947
14	245251.6	3361812H1	686	947
14	245251.6	4349129H1	686	875
14	245251.6	4847891H1	686	922
14	245251.6	929615H1	686	943
14	245251.6	4593502H1	686	938
14	245251.6	g1956732	701	948
14	245251.6	3325687H2	554	664
14	245251.6	1504636H1	699	951
14	245251.6	3357413H1	686	931
14	245251.6	2093969H1	7	120
14	245251.6	3888045H1	686	917
14	245251.6	4400406H1	704	949
14	245251.6	4675188H1	686	895
14	245251.6	1833267H1	696	949

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SEQ ID NO:	Template ID	Component ID	Start	Stop
14	245251.6	3531646H1	1290	1419
14	245251.6	4675103H1	686	823
14	245251.6	612029H1	686	948
14	245251.6	g3861897	1283	1417
14	245251.6	g3861915	10	142
14	245251.6	4585634H1	686	807
14	245251.6	g1187227	736	954
14	245251.6	g3806416	6	142
14	245251.6	g809795	688	920
14	245251.6	g3806236	1283	1417
14	245251.6	5184838H1	686	929
14	245251.6	g3806383	9	142
14	245251.6	g3862381	6	142
14	245251.6	5102972H1	686	938
14	245251.6	g3806305	1283	1416
14	245251.6	4049171H1	686	952
14	245251.6	5399585H1	686	806
14	245251.6	g3806377	8	142
14	245251.6	1609289H1	686	861
14	245251.6	g1985106	688	952
14	245251.6	1631116H1	740	958
14	245251.6	g3846850	1283	1419
14	245251.6	3371627H1	686	934
14	245251.6	g3842256	1283	1415
14	245251.6	g1948393	686	952
14	245251.6	g3849535	8	142
14	245251.6	1353725H1	686	906
14	245251.6	3811303H1	395	637
14	245251.6	g3849274	1283	1417
14	245251.6	770658H1	692	958
14	245251.6	1709346H1	686	889
14	245251.6	g3923055	1283	1416
14	245251.6	1351272H1	686	917
14	245251.6	2497443H1	686	952
14	245251.6	6007158H1	686	958
14	245251.6	g4086359	1283	1419
14	245251.6	g3849526	1283	1419
14	245251.6	5905094H1	686	959
14	245251.6	g3847515	1283	1417
14	245251.6	3040561H1	686	954
14	245251.6	1886946H1	686	956
14	245251.6	4764852H1	686	958
14	245251.6	g3847084	1283	1417
14	245251.6	g3845943	1283	1419
14	245251.6	5685528H1	686	956
14	245251.6	g3846660	9	142
14	245251.6	g3845949	1283	1419
14	245251.6	3400315H1	688	927
14	245251.6	g1953701	688	939
14	245251.6	5833060H1	686	954

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SEQ ID NO:	Template ID	Component ID	Start	Stop
14	245251.6	g3989265	1283	1417
14	245251.6	4049178H1	686	954
14	245251.6	g2038078	686	957
14	245251.6	212969H1	686	851
14	245251.6	g4074607	9	142
14	245251.6	g3990111	1283	1419
14	245251.6	4265942H1	688	945
14	245251.6	g3990156	1283	1415
14	245251.6	1859765H1	446	666
14	245251.6	g3847576	9	142
14	245251.6	g1320366	594	1041
14	245251.6	2039935H1	596	882
14	245251.6	5299657H1	601	870
14	245251.6	4947763H1	623	800
14	245251.6	799795H1	640	890
14	245251.6	g1957419	644	1200
14	245251.6	1503008H1	669	974
14	245251.6	1503133H1	669	1024
14	245251.6	1703102H1	670	907
14	245251.6	5945265H1	671	965
14	245251.6	4154972H1	672	973
14	245251.6	4783070H1	677	947
14	245251.6	2729061H1	680	956
14	245251.6	4817713H1	683	981
14	245251.6	2604603H1	685	958
14	245251.6	2300089H1	685	963
14	245251.6	3647926H1	689	1020
14	245251.6	5120725H1	690	1026
14	245251.6	083810H1	692	952
14	245251.6	4409416H1	694	881
14	245251.6	4057228H1	694	996
14	245251.6	5395048H1	696	1005
14	245251.6	3481334H1	693	1055
14	245251.6	4218418H1	694	988
14	245251.6	4820226H1	695	855
14	245251.6	4073954H1	694	1017
14	245251.6	1315458H1	695	975
14	245251.6	3600571H1	696	1025
14	245251.6	3776260H1	696	1029
14	245251.6	3588749H1	695	1055
14	245251.6	2814583F6	696	1360
14	245251.6	1229362H1	696	948
14	245251.6	5732270H1	695	982
14	245251.6	g1727842	696	1088
14	245251.6	3660326H1	696	915
14	245251.6	4198443H1	697	808
14	245251.6	1455236H1	695	976
14	245251.6	2343111H1	696	992
14	245251.6	3513953H1	696	992
14	245251.6	4999458H1	696	993

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SEQ ID NO:	Template ID	Component ID	Start	Stop
14	245251.6	2261362H1	696	975
14	245251.6	3029907H1	696	1017
14	245251.6	5121569H1	696	1011
14	245251.6	4537506H1	695	979
14	245251.6	3321759H1	696	1013
14	245251.6	2307802H1	697	981
14	245251.6	2307804H1	697	979
14	245251.6	3012456H1	697	951
14	245251.6	2504610H1	697	952
14	245251.6	3362687H1	697	990
14	245251.6	3748602H1	696	901
14	245251.6	3316419H1	697	990
14	245251.6	2814582H1	696	992
14	245251.6	2272892H1	697	993
14	245251.6	1807854H1	696	976
14	245251.6	g2466185	697	1219
14	245251.6	2132022H1	697	996
14	245251.6	2132022R6	697	1408
14	245251.6	3073883H1	697	997
14	245251.6	2125224H1	697	1003
14	245251.6	2269903H1	697	816
14	245251.6	1459722H1	697	922
14	245251.6	4562893H1	697	981
14	245251.6	1496792H1	696	922
14	245251.6	5221884H2	697	975
14	245251.6	5572366H1	697	928
14	245251.6	2771241H1	697	967
14	245251.6	1573610H1	697	974
14	245251.6	1867126H1	697	1002
14	245251.6	1507375H1	697	928
14	245251.6	1573473H1	697	932
14	245251.6	3267774H1	697	1002
14	245251.6	3163705H1	697	973
14	245251.6	3272193H1	696	970
14	245251.6	2985313H1	697	1009
14	245251.6	3495519H1	697	1014
14	245251.6	3943155H1	697	981
14	245251.6	3812545H1	697	1032
14	245251.6	2708787H1	697	1024
14	245251.6	3639075H1	697	1030
14	245251.6	g1940776	733	1099
14	245251.6	g908409	734	1122
14	245251.6	5865030H1	736	1078
14	245251.6	4050960H1	736	1049
14	245251.6	3819250H1	751	1088
14	245251.6	g1761139	757	1219
14	245251.6	g1967349	756	1382
14	245251.6	g1618353	729	1108
14	245251.6	g1364436	729	1251
14	245251.6	g1727492	715	1095

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
14	245251.6	g1968929	710	1184
14	245251.6	5161050F6	712	1306
14	245251.6	g1959923	712	1159
14	245251.6	g1757908	715	1152
14	245251.6	1229535H1	721	817
14	245251.6	1844975H1	725	1044
14	245251.6	g1295958	729	1461
14	245251.6	358108H1	712	839
14	245251.6	2903511H1	712	1072
14	245251.6	3087812H1	712	1032
14	245251.6	g1440940	728	1227
15	252875.1	2931079H1	2777	3055
15	252875.1	1917962H1	2777	2996
15	252875.1	827946H1	2777	3031
15	252875.1	g1494002	2777	2956
15	252875.1	1452450H1	2777	2989
15	252875.1	g28465	2777	2913
15	252875.1	g2046620	2785	3270
15	252875.1	g897974	2789	3046
15	252875.1	4584285H1	2789	3086
15	252875.1	g897962	2789	3132
15	252875.1	5518734H1	2797	3022
15	252875.1	g1157691	2797	3093
15	252875.1	5587262H1	2798	3081
15	252875.1	1547554H1	2800	2940
15	252875.1	2169571H1	2840	3091
15	252875.1	5449334H1	2849	3116
15	252875.1	4340677H1	2859	3171
15	252875.1	3015019H1	2858	3160
15	252875.1	406486H1	2859	3107
15	252875.1	3556907H1	2862	3187
15	252875.1	2651443H1	2871	3120
15	252875.1	2444851H1	2875	3115
15	252875.1	373627H1	2876	3096
15	252875.1	2172734H1	2879	3083
15	252875.1	5875371H1	2881	3171
15	252875.1	g1690763	2890	3247
15	252875.1	g1506919	2890	3158
15	252875.1	3842658H1	2897	3209
15	252875.1	4435381H1	2895	3130
15	252875.1	2799807H1	2897	3164
15	252875.1	2909321H1	2904	3055
15	252875.1	3093958H1	2913	3222
15	252875.1	4644257H1	2913	3192
15	252875.1	2594951H1	2918	3182
15	252875.1	720109H1	2928	3197
15	252875.1	531590H1	2932	3153
15	252875.1	5497370H1	2938	3133
15	252875.1	4741744H1	2940	3237
15	252875.1	2850778H1	2951	3229

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
15	252875.1	2420169H1	2950	3197
15	252875.1	2227025H1	2953	3202
15	252875.1	1948888H1	2953	3118
15	252875.1	967671R1	2957	3598
15	252875.1	2682662H1	2956	3270
15	252875.1	967671H1	2957	3272
15	252875.1	g1303166	2964	3269
15	252875.1	4323462H1	2975	3231
15	252875.1	3774157H1	2982	3300
15	252875.1	2384295H2	2984	3216
15	252875.1	4156648H1	2992	3290
15	252875.1	5373633H1	2994	3209
15	252875.1	190297H1	3005	3261
15	252875.1	190297R1	3005	3659
15	252875.1	3222225H1	3006	3362
15	252875.1	2197579H1	3012	3284
15	252875.1	4334641H1	3016	3321
15	252875.1	1739115H1	3031	3225
15	252875.1	2076112H1	3031	3345
15	252875.1	4588978H1	3031	3144
15	252875.1	1929325H1	3033	3287
15	252875.1	1698356H1	3044	3278
15	252875.1	774049H1	3044	3278
15	252875.1	3201988H1	3045	3229
15	252875.1	g1165436	3045	3537
15	252875.1	4079815H1	3046	3338
15	252875.1	546658H1	3054	3386
15	252875.1	3243004H1	3061	3315
15	252875.1	2285730H1	3074	3327
15	252875.1	4957381H1	3075	3353
15	252875.1	g1165609	3101	3371
15	252875.1	548503H1	3112	3289
15	252875.1	434752H1	3117	3345
15	252875.1	1665374H1	3115	3374
15	252875.1	3766307H1	3116	3255
15	252875.1	5301677H1	3118	3294
15	252875.1	619409H1	3124	3411
15	252875.1	2134475H1	3129	3401
15	252875.1	1328119H1	3134	3432
15	252875.1	g835219	3135	3529
15	252875.1	3414825H1	3663	3915
15	252875.1	g4285757	3666	3843
15	252875.1	3992325H1	3673	3977
15	252875.1	1684593H1	3674	3906
15	252875.1	g1690764	3683	3831
15	252875.1	507054H1	3693	3932
15	252875.1	g1493946	3705	3840
15	252875.1	2113227H1	3709	4000
15	252875.1	g4457753	3711	3844
15	252875.1	1601661H1	3712	3926

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
15	252875.1	5860245H1	3714	4016
15	252875.1	g897528	3724	3841
15	252875.1	g1149324	3726	3877
15	252875.1	731353H1	3733	3998
15	252875.1	5219557H1	3737	3928
15	252875.1	g1194254	3752	4014
15	252875.1	g1976483	3768	4129
15	252875.1	g1194793	3775	3940
15	252875.1	3806345H1	3781	4050
15	252875.1	2603535H1	3783	4049
15	252875.1	4766360H1	3785	4070
15	252875.1	1833291H1	3783	4043
15	252875.1	3450113H1	3790	4072
15	252875.1	5120311H1	634	940
15	252875.1	2866935H1	741	1043
15	252875.1	638818H1	752	1017
15	252875.1	3435566H1	812	1068
15	252875.1	2169234H1	833	1056
15	252875.1	2169234F6	833	1253
15	252875.1	5636183H1	906	1181
15	252875.1	4267043H1	961	1243
15	252875.1	3416556H1	985	1240
15	252875.1	5502666H1	1070	1287
15	252875.1	g1384448	1072	1421
15	252875.1	4698366H1	1099	1361
15	252875.1	2477291H1	1137	1358
15	252875.1	1274557F6	1172	1609
15	252875.1	1274557H1	1172	1419
15	252875.1	g3845885	1226	1585
15	252875.1	2746276H1	1241	1484
15	252875.1	3488583H1	1249	1508
15	252875.1	g2557990	1259	1550
15	252875.1	g3412243	1271	1590
15	252875.1	g2013979	1289	1524
15	252875.1	g2217748	4188	4593
15	252875.1	1336165H1	4186	4455
15	252875.1	2803030H1	4193	4486
15	252875.1	3728371H1	4193	4534
15	252875.1	g2195154	4193	4593
15	252875.1	3728371T1	4203	4554
15	252875.1	g1192650	4206	4590
15	252875.1	g2279223	4215	4590
15	252875.1	2718529H1	4217	4515
15	252875.1	g3229683	4218	4587
15	252875.1	g3144363	4227	4593
15	252875.1	g1891729	4233	4590
15	252875.1	g3666365	4234	4594
15	252875.1	g3742308	4240	4593
15	252875.1	709764H1	4243	4529
15	252875.1	g3237786	4245	4587

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
15	252875.1	g1545463	4245	4602
15	252875.1	g2840952	4251	4587
15	252875.1	g2883750	4267	4608
15	252875.1	224311H1	4280	4486
15	252875.1	224311F1	4280	4587
15	252875.1	226928H1	4280	4545
15	252875.1	229979H1	4280	4508
15	252875.1	4091574H1	4282	4578
15	252875.1	2887836H1	4282	4576
15	252875.1	g4326366	4283	4593
15	252875.1	g1139072	4293	4594
15	252875.1	g3434294	4294	4587
15	252875.1	1740259R6	4294	4587
15	252875.1	1740259H1	4294	4532
15	252875.1	1740259T6	4294	4553
15	252875.1	3470373H1	4300	4587
15	252875.1	g4149411	4304	4593
15	252875.1	659699H1	4310	4590
15	252875.1	731353F1	4156	4587
15	252875.1	g1846732	4157	4593
15	252875.1	g3214922	4160	4594
15	252875.1	g3416272	4325	4587
15	252875.1	g4525092	4330	4596
15	252875.1	4423707H1	4332	4587
15	252875.1	g3428976	4162	4595
15	252875.1	g3895874	4162	4596
15	252875.1	224311R1	4177	4587
15	252875.1	g2753953	4168	4587
15	252875.1	g1626194	4171	4595
15	252875.1	g3146324	4171	4542
15	252875.1	g2779866	4172	4504
15	252875.1	g2054706	3495	3840
15	252875.1	3837481H1	3497	3712
15	252875.1	3512137H1	3510	3600
15	252875.1	g566011	3510	3833
15	252875.1	3325564H1	3518	3685
15	252875.1	g2537480	3527	4057
15	252875.1	2586362H1	3531	3819
15	252875.1	1265894H1	3534	3772
15	252875.1	1265894F1	3534	4149
15	252875.1	g1271274	3538	3812
15	252875.1	4339850H1	3540	3823
15	252875.1	5014329H1	3540	3807
15	252875.1	g4333060	3540	3830
15	252875.1	g3899484	3542	3840
15	252875.1	4019833H1	3553	3873
15	252875.1	3930433H1	3553	3868
15	252875.1	1394247H1	3557	3830
15	252875.1	g670185	3558	3833
15	252875.1	g897537	3565	3831

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
15	252875.1	2313534H1	3569	3818
15	252875.1	1258470F1	3572	4196
15	252875.1	g4304393	3571	3842
15	252875.1	2692250H1	3572	3831
15	252875.1	1258470H1	3572	3836
15	252875.1	g1275416	3572	4230
15	252875.1	3809069H1	3582	3895
15	252875.1	g1152594	3583	3840
15	252875.1	g2321801	3588	3838
15	252875.1	g835206	3590	3840
15	252875.1	2808212H1	3607	3935
15	252875.1	1916784H1	3616	3905
15	252875.1	1251826H1	3619	3778
15	252875.1	1251826F1	3619	3830
15	252875.1	g3920452	2265	2604
15	252875.1	2457404H1	2267	2520
15	252875.1	5216436H1	2268	2523
15	252875.1	g572819	2271	2614
15	252875.1	2685979H1	2291	2546
15	252875.1	4311421H1	2289	2413
15	252875.1	1387882H1	2291	2569
15	252875.1	1994174H1	2291	2402
15	252875.1	1386461H1	2291	2425
15	252875.1	3296980H1	2293	2560
15	252875.1	3742330H1	2307	2605
15	252875.1	2839295H1	2309	2585
15	252875.1	2615762H1	2321	2606
15	252875.1	2115669H1	2327	2594
15	252875.1	3248377H1	2331	2428
15	252875.1	1892380H1	2352	2493
15	252875.1	g2217857	2382	2726
15	252875.1	3425510H1	2390	2665
15	252875.1	3666290H1	2391	2590
15	252875.1	3133325H1	2392	2667
15	252875.1	g1897668	2395	2756
15	252875.1	034289H1	2400	2657
15	252875.1	g1062015	2406	2733
15	252875.1	3542538H1	2407	2673
15	252875.1	3542586H1	2407	2668
15	252875.1	2969209H1	2424	2686
15	252875.1	4358014H1	2434	2716
15	252875.1	3657619H1	2435	2724
15	252875.1	g2930924	2236	2642
15	252875.1	031953H1	2440	2723
15	252875.1	030691H1	2440	2652
15	252875.1	g1154198	2441	2728
15	252875.1	2069257T6	2441	2867
15	252875.1	2744591H1	2441	2699
15	252875.1	g1062277	2451	2739
15	252875.1	1945843H1	2476	2722

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
15	252875.1	5135194H1	2479	2749
15	252875.1	4173923H1	2497	2797
15	252875.1	1853266H1	2497	2756
15	252875.1	5542442H1	2499	2719
15	252875.1	5497660H1	2514	2768
15	252875.1	g4086589	2517	2925
15	252875.1	5878048H1	2521	2830
15	252875.1	g1320612	2521	2852
15	252875.1	3891146H1	2524	2756
15	252875.1	2073038H1	2529	2756
15	252875.1	5834734H1	2544	2775
15	252875.1	5512348H1	2569	2872
15	252875.1	5512133H1	2569	2756
15	252875.1	1996543R6	2578	3088
15	252875.1	1996543H1	2578	2842
15	252875.1	3940668H1	2587	2874
15	252875.1	060574H1	2591	2756
15	252875.1	4151473H1	2591	2870
15	252875.1	5196676H1	2591	2860
15	252875.1	030354H1	2599	2860
15	252875.1	4196058H1	2603	2923
15	252875.1	1450989F1	2621	2982
15	252875.1	1450989H1	2621	2901
15	252875.1	g2218312	2632	3002
15	252875.1	g1383259	2632	3083
15	252875.1	g2617741	2633	2835
15	252875.1	g791689	2635	2874
15	252875.1	4933134H1	2648	2964
15	252875.1	2797213H1	2678	2953
15	252875.1	4864853H1	2678	2935
15	252875.1	2798634H1	2678	2946
15	252875.1	633892H1	2688	2918
15	252875.1	g880789	2705	3081
15	252875.1	2807841H1	2737	3068
15	252875.1	g1182637	2746	3090
15	252875.1	g1125575	2753	3131
15	252875.1	g1295159	2765	3081
15	252875.1	4265522H1	2774	3018
15	252875.1	900222R1	2775	3209
15	252875.1	900222H1	2775	3120
15	252875.1	4410765H1	2777	2983
15	252875.1	3468239H1	2777	2966
15	252875.1	2551180H1	2777	2970
15	252875.1	3813780H1	2777	3065
15	252875.1	g1506871	3620	3830
15	252875.1	g791584	3621	3848
15	252875.1	2407631H1	3621	3840
15	252875.1	g835220	3629	3841
15	252875.1	g3038977	3629	3783
15	252875.1	g1062367	3637	3823

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
15	252875.1	310441H1	3639	3825
15	252875.1	310441R6	3640	3924
15	252875.1	4080535H1	3641	3961
15	252875.1	1740495H1	3641	3892
15	252875.1	4647311H1	3642	3919
15	252875.1	388848H1	3647	3848
15	252875.1	g1332310	3651	4188
15	252875.1	g1332258	3651	4126
15	252875.1	g1524775	3653	4182
15	252875.1	g1443183	3652	3840
15	252875.1	g1891789	3654	4121
15	252875.1	400845H1	3659	3849
15	252875.1	2639596H1	1369	1429
15	252875.1	2874502F6	1406	1784
15	252875.1	2169234T6	1331	1696
15	252875.1	2874502H1	1407	1686
15	252875.1	2746872H1	1408	1674
15	252875.1	g1984049	1443	1765
15	252875.1	5264513F6	1452	1772
15	252875.1	g2526630	1461	1904
15	252875.1	2877577H1	1498	1668
15	252875.1	2871627H1	1498	1758
15	252875.1	4768331H1	1519	1790
15	252875.1	2762166H1	1536	1793
15	252875.1	g2010681	1598	1898
15	252875.1	5370588H1	1609	1832
15	252875.1	3725509H1	1646	1936
15	252875.1	4714478H1	1664	1929
15	252875.1	1950683H1	1674	1901
15	252875.1	g2006648	1675	1920
15	252875.1	g2027521	1714	2070
15	252875.1	3825837H1	1735	2021
15	252875.1	g4511067	1738	2020
15	252875.1	653234H1	1780	2029
15	252875.1	2170628H1	1806	2054
15	252875.1	2170628F6	1806	2302
15	252875.1	1665096H1	1845	2078
15	252875.1	5695708H1	1860	2097
15	252875.1	g573675	1919	2227
15	252875.1	5638872H1	1975	2241
15	252875.1	5086872H1	1983	2207
15	252875.1	1689519H1	1988	2112
15	252875.1	4833076H1	1999	2262
15	252875.1	3370367H1	2005	2286
15	252875.1	2354679H1	2006	2135
15	252875.1	g2011403	2014	2239
15	252875.1	4820085H1	2037	2264
15	252875.1	6063612H1	2037	2310
15	252875.1	2170628T6	2050	2471
15	252875.1	g3676979	2051	2516

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
15	252875.1	4346524H1	2081	2351
15	252875.1	2650068H1	2081	2333
15	252875.1	059589H1	2091	2303
15	252875.1	g2335474	2135	2520
15	252875.1	g616509	2166	2506
15	252875.1	4993749H1	2166	2461
15	252875.1	729898H1	2167	2371
15	252875.1	729898R6	2167	2582
15	252875.1	730915R6	2167	2686
15	252875.1	729898R1	2167	2512
15	252875.1	350527H1	2181	2315
15	252875.1	1486345H1	2211	2463
15	252875.1	1486345F6	2211	2586
15	252875.1	5450622H1	2228	2489
15	252875.1	4553123H1	3172	3443
15	252875.1	3629790H1	3181	3496
15	252875.1	402268H1	3188	3407
15	252875.1	1509841H1	3195	3397
15	252875.1	1509833H1	3195	3399
15	252875.1	4919221H1	3206	3499
15	252875.1	g835205	3135	3437
15	252875.1	4073386H1	3142	3458
15	252875.1	2445427H1	3156	3414
15	252875.1	2041560H1	3157	3451
15	252875.1	5013650H1	3219	3526
15	252875.1	1876087H1	3222	3480
15	252875.1	2401949H1	3222	3494
15	252875.1	5875179H1	3223	3506
15	252875.1	5518081H1	3236	3414
15	252875.1	3163335H1	3239	3533
15	252875.1	5636648H1	3241	3536
15	252875.1	3076681H1	3247	3407
15	252875.1	g3850466	3246	3697
15	252875.1	1876575H1	3254	3547
15	252875.1	g1367750	3257	3843
15	252875.1	4931430H1	3264	3545
15	252875.1	1958432H1	3269	3585
15	252875.1	627261H1	3274	3529
15	252875.1	3786347H1	3281	3554
15	252875.1	1730878H1	3283	3539
15	252875.1	1730895H1	3283	3490
15	252875.1	1730824H1	3283	3492
15	252875.1	2874502T6	3290	3797
15	252875.1	469285H1	3293	3550
15	252875.1	2058867H1	3298	3571
15	252875.1	2058867R6	3298	3699
15	252875.1	5733018H1	3300	3592
15	252875.1	1261341H1	3301	3574
15	252875.1	2878759H1	3307	3607
15	252875.1	1398976H1	3310	3559

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
15	252875.1	g1751344	3316	3586
15	252875.1	720109F1	3317	3840
15	252875.1	g2945397	3332	3840
15	252875.1	5778084H1	3336	3617
15	252875.1	g767808	3337	3845
15	252875.1	5777985H1	3337	3574
15	252875.1	1337062H1	3340	3594
15	252875.1	g3280387	3347	3842
15	252875.1	2289425H1	3347	3610
15	252875.1	g3675613	3354	3840
15	252875.1	3801180H1	3355	3524
15	252875.1	2876933H1	3367	3502
15	252875.1	g4269890	3369	3846
15	252875.1	952792T1	3382	3758
15	252875.1	2409980H1	3383	3623
15	252875.1	g3446123	3389	3840
15	252875.1	g2930114	3390	3850
15	252875.1	g1157245	3394	3841
15	252875.1	1880890H1	3392	3654
15	252875.1	952792R1	3394	3843
15	252875.1	952792H1	3396	3588
15	252875.1	g3988283	3397	3840
15	252875.1	1813653H1	3396	3598
15	252875.1	1213928H1	3398	3638
15	252875.1	1213928T1	3398	3797
15	252875.1	g3872611	3405	3840
15	252875.1	2505231H1	3406	3652
15	252875.1	g4452830	3407	3840
15	252875.1	g4523040	3407	3840
15	252875.1	g1897843	3408	3844
15	252875.1	4715628H1	3411	3673
15	252875.1	2994530H1	3411	3680
15	252875.1	661001R6	3412	3843
15	252875.1	g3422408	3412	3840
15	252875.1	660905H1	3412	3685
15	252875.1	g3870520	3412	3840
15	252875.1	661001T6	3412	3798
15	252875.1	660690H1	3412	3692
15	252875.1	1740390H1	3414	3649
15	252875.1	3773806H1	3416	3738
15	252875.1	g1324229	3421	3969
15	252875.1	g3433983	3430	3849
15	252875.1	g1440537	3440	3737
15	252875.1	g1545520	3441	3877
15	252875.1	g2264856	3445	3842
15	252875.1	g2968893	3446	3844
15	252875.1	3972857H1	3449	3612
15	252875.1	3521680H1	3446	3813
15	252875.1	475000H1	3459	3741
15	252875.1	1369528H1	3462	3711

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
15	252875.1	4716618H1	3464	3764
15	252875.1	5402888H1	3470	3744
15	252875.1	737350H1	3473	3678
15	252875.1	149929H1	3479	3686
15	252875.1	149929R1	3478	4058
15	252875.1	2746121H1	3479	3733
15	252875.1	g1060820	3490	3824
15	252875.1	862523R1	3492	4121
15	252875.1	862523H1	3492	3770
15	252875.1	1741284H1	3492	3722
15	252875.1	1578142H1	3496	3744
15	252875.1	1962956H1	3795	4112
15	252875.1	5186635H1	3795	4047
15	252875.1	2110916H1	3795	3950
15	252875.1	2870075H1	3798	4092
15	252875.1	872794R1	3800	4322
15	252875.1	872794H1	3800	4089
15	252875.1	3560953H1	3801	4004
15	252875.1	3623917H1	3811	3995
15	252875.1	4176710H1	3809	4014
15	252875.1	2364402H1	3813	3996
15	252875.1	2017186H1	3822	4091
15	252875.1	2806941H1	3825	4141
15	252875.1	1364748R1	3836	4363
15	252875.1	1364748H1	3836	4115
15	252875.1	2126618H1	3840	4142
15	252875.1	2058867T6	3849	4554
15	252875.1	1268579H1	3853	4104
15	252875.1	2420031H1	3861	4111
15	252875.1	867120H1	3861	4022
15	252875.1	3471449H1	3865	4144
15	252875.1	310441T6	3890	4550
15	252875.1	687562H1	3894	4173
15	252875.1	5022130T1	3901	4543
15	252875.1	4995018H1	3907	4179
15	252875.1	5022130H1	3906	4031
15	252875.1	5401446H1	3913	4169
15	252875.1	3279479H1	3926	4204
15	252875.1	1517039H1	3926	4149
15	252875.1	1517087H1	3926	4130
15	252875.1	2072072H1	3934	4206
15	252875.1	3781502H1	3941	4286
15	252875.1	1548234H1	3941	4170
15	252875.1	5390212H1	3942	4216
15	252875.1	g1321347	3949	4364
15	252875.1	3092282H1	3956	4209
15	252875.1	320547H1	3969	4394
15	252875.1	4436308H1	3979	4256
15	252875.1	1901926H1	3988	4270
15	252875.1	3051460H1	3988	4292

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
15	252875.1	3836484H1	4000	4290
15	252875.1	2423168H1	4010	4263
15	252875.1	4122620H1	4011	4292
15	252875.1	149929F1	4015	4587
15	252875.1	1590154H1	4014	4284
15	252875.1	779159H1	4016	4273
15	252875.1	779159R1	4016	4586
15	252875.1	4718944H1	4016	4296
15	252875.1	4981471H1	4019	4227
15	252875.1	2128923H1	4025	4308
15	252875.1	3859444H1	4027	4310
15	252875.1	3856453H1	4027	4286
15	252875.1	2564780H1	4029	4155
15	252875.1	5911630H1	4042	4395
15	252875.1	730915T6	4045	4555
15	252875.1	g2619417	4049	4327
15	252875.1	g2619632	4050	4332
15	252875.1	729898T6	4065	4551
15	252875.1	1667393H1	4074	4312
15	252875.1	4339273H1	4072	4385
15	252875.1	1666593H1	4074	4303
15	252875.1	1667396H1	4074	4312
15	252875.1	g1846687	4080	4520
15	252875.1	g4108324	4089	4587
15	252875.1	2736196H1	4093	4366
15	252875.1	2736715H1	4093	4373
15	252875.1	3879868H1	4100	4235
15	252875.1	g3675575	4102	4587
15	252875.1	g1332311	4107	4604
15	252875.1	g4329975	4102	4587
15	252875.1	g1524714	4104	4600
15	252875.1	g3278422	4104	4587
15	252875.1	g3596503	4106	4587
15	252875.1	g2656299	4107	4592
15	252875.1	1759044H1	4108	4370
15	252875.1	3951189H1	4107	4428
15	252875.1	g4393268	4109	4596
15	252875.1	g3920837	4110	4593
15	252875.1	3559291H1	4111	4437
15	252875.1	g3644402	4116	4596
15	252875.1	5683481H1	4117	4371
15	252875.1	g3238075	4121	4587
15	252875.1	g1219850	4128	4589
15	252875.1	2599386H1	4126	4428
15	252875.1	g2217641	4128	4592
15	252875.1	g4394253	4129	4587
15	252875.1	g4267736	4136	4589
15	252875.1	g4453805	4139	4593
15	252875.1	g4522737	4140	4593
15	252875.1	g1332201	4155	4593

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SEQ ID NO:	Template ID	Component ID	Start	Stop
15	252875.1	g4509608	4154	4593
15	252875.1	5614003H1	4156	4396
15	252875.1	g4243557	4155	4593
15	252875.1	2754555H1	4338	4593
15	252875.1	g879867	4365	4600
15	252875.1	g1266259	4368	4594
15	252875.1	3327329H1	4370	4597
15	252875.1	4248607H1	4392	4609
15	252875.1	g4186572	4402	4587
15	252875.1	1351626H1	4411	4567
15	252875.1	1351626F1	4411	4587
15	252875.1	302767H1	4412	4588
15	252875.1	1968509H1	4412	4594
15	252875.1	5876201H1	4413	4603
15	252875.1	g2433592	4416	4598
15	252875.1	2969615H1	4419	4563
15	252875.1	g2942070	4469	4587
15	252875.1	g1267224	4474	4593
15	252875.1	2043678H1	4475	4587
15	252875.1	g2986396	4477	4587
15	252875.1	3373314H1	1	112
15	252875.1	3077972H1	5	316
15	252875.1	2069257H1	42	277
15	252875.1	3073491H1	42	295
15	252875.1	2069257F6	47	450
15	252875.1	482316H1	49	258
15	252875.1	3036127H1	49	267
15	252875.1	3607250H1	49	197
15	252875.1	3343670H1	49	258
15	252875.1	3394626H1	49	291
15	252875.1	5522114H1	68	242
15	252875.1	3419860H1	176	401
15	252875.1	3199647H1	305	401
15	252875.1	g1984204	369	786
15	252875.1	3536255H1	386	662
15	252875.1	3528024H1	563	799
16	252964.2	4178741H1	3001	3238
16	252964.2	830538H1	3012	3108
16	252964.2	830538T1	3012	3198
16	252964.2	830538R1	3012	3238
16	252964.2	g3057275	3033	3241
16	252964.2	g1164549	3040	3238
16	252964.2	g1894136	3044	3243
16	252964.2	747073H1	3055	3313
16	252964.2	4074768H1	3099	3217
16	252964.2	g863600	3102	3226
16	252964.2	g1060375	3108	3215
16	252964.2	g1892056	3109	3241
16	252964.2	g2620960	3140	3245
16	252964.2	g3805026	3150	3252

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
16	252964.2	2939591H1	2679	2990
16	252964.2	1993076T6	2681	3200
16	252964.2	221873H1	2702	2925
16	252964.2	2853281H1	2711	3001
16	252964.2	2260511H1	2723	2995
16	252964.2	5289957H1	2723	3020
16	252964.2	g868647	2723	3063
16	252964.2	g3108721	2731	3238
16	252964.2	4381077H1	2740	3027
16	252964.2	5272939H1	2740	3013
16	252964.2	g2161092	2743	3241
16	252964.2	3223031H1	2758	2944
16	252964.2	1843518H1	2758	3072
16	252964.2	2245609H1	2779	3073
16	252964.2	g820162	2779	3063
16	252964.2	g3033754	2784	3244
16	252964.2	4642653H1	2785	3057
16	252964.2	g3900624	2787	3243
16	252964.2	g4267231	2793	3238
16	252964.2	g3919071	2794	3238
16	252964.2	2188192H1	2810	3110
16	252964.2	2369459T6	2816	3198
16	252964.2	450871T6	2828	3200
16	252964.2	661201H1	2842	3123
16	252964.2	5594903H1	2842	3112
16	252964.2	2736768H1	2850	3140
16	252964.2	g3870375	2856	3243
16	252964.2	3805033H1	2856	3172
16	252964.2	g4330626	2857	3238
16	252964.2	g4112946	2862	3238
16	252964.2	4540882H1	2889	3156
16	252964.2	g2207247	2889	3238
16	252964.2	g2218580	2889	3250
16	252964.2	g1719392	2892	3239
16	252964.2	1833491H1	2896	3197
16	252964.2	911307H1	2899	3168
16	252964.2	619933H1	2906	3185
16	252964.2	g3960791	2916	3238
16	252964.2	g4391406	2917	3247
16	252964.2	g2715745	2919	3238
16	252964.2	g4268192	2920	3241
16	252964.2	g4267270	2921	3244
16	252964.2	g3644389	2922	3247
16	252964.2	928993H1	2924	3085
16	252964.2	g2903695	2930	3238
16	252964.2	g566929	2935	3238
16	252964.2	g1153963	2967	3238
16	252964.2	3116982H1	2660	2957
16	252964.2	g4070514	2973	3243
16	252964.2	2792353H1	2660	2757

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
16	252964.2	g3778735	2983	3238
16	252964.2	053091H1	2997	3206
16	252964.2	497154H1	2999	3190
16	252964.2	500461H1	2999	3218
16	252964.2	2673105H1	1792	2031
16	252964.2	5855988H1	1793	2040
16	252964.2	5118330H1	1803	2082
16	252964.2	2866056H1	1860	2172
16	252964.2	4851249H1	1893	2144
16	252964.2	5007337H1	1898	2151
16	252964.2	g1719391	1899	2291
16	252964.2	2227319H1	1903	2148
16	252964.2	5926595H1	1920	2214
16	252964.2	g1060485	1945	2361
16	252964.2	2845135H1	1958	2191
16	252964.2	1913383H1	2031	2290
16	252964.2	3481001H1	2073	2222
16	252964.2	5403224H1	2075	2379
16	252964.2	2370791H1	2076	2304
16	252964.2	2370791F6	2076	2562
16	252964.2	3234460H1	2083	2331
16	252964.2	g1273052	2102	2564
16	252964.2	4849809H1	2102	2386
16	252964.2	3551288H1	2110	2331
16	252964.2	6065193H1	2112	2375
16	252964.2	805687R1	2130	2640
16	252964.2	805687H1	2140	2339
16	252964.2	4818872H1	2168	2338
16	252964.2	445589H1	2169	2424
16	252964.2	3534641H1	2170	2472
16	252964.2	4932921H1	2228	2496
16	252964.2	g1187975	2229	2592
16	252964.2	925326H1	2237	2551
16	252964.2	925389H1	2237	2337
16	252964.2	925326R1	2238	2597
16	252964.2	1984547H1	2246	2523
16	252964.2	1984547R6	2246	2718
16	252964.2	822651H1	2256	2524
16	252964.2	822651R1	2256	2803
16	252964.2	2960302H1	2287	2582
16	252964.2	2745337H1	2311	2556
16	252964.2	2745683H1	2311	2554
16	252964.2	5015696H1	2321	2422
16	252964.2	5552559H1	2322	2586
16	252964.2	3469448H1	2323	2579
16	252964.2	4834907H1	2329	2586
16	252964.2	785664H1	2331	2633
16	252964.2	785664R6	2331	2771
16	252964.2	785257R1	2331	2862
16	252964.2	785257H1	2331	2582

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
16	252964.2	4266319H1	2385	2565
16	252964.2	g2161091	2394	2814
16	252964.2	3021996H1	2395	2694
16	252964.2	4795127H1	2428	2695
16	252964.2	1427976H1	2443	2707
16	252964.2	1427976F6	2443	3025
16	252964.2	002126H1	2461	2923
16	252964.2	g1783079	2462	2847
16	252964.2	g1892162	2462	2884
16	252964.2	4593447H1	2479	2737
16	252964.2	4416604H1	2486	2723
16	252964.2	313687H1	2491	2731
16	252964.2	374457H1	2492	2707
16	252964.2	1231088H1	2511	2737
16	252964.2	1427976T6	2510	3060
16	252964.2	2421408H1	2535	2775
16	252964.2	1237191H1	2545	2782
16	252964.2	1237191F1	2545	3125
16	252964.2	2564135H1	2568	2835
16	252964.2	1364705H1	2569	2836
16	252964.2	1364705R1	2569	2936
16	252964.2	2570283H1	2569	2830
16	252964.2	3811167H1	2577	2851
16	252964.2	g3958470	2603	3096
16	252964.2	785664T6	2611	3198
16	252964.2	6103263H1	2623	2913
16	252964.2	g2207504	2652	3049
16	252964.2	2820307H1	2657	3013
16	252964.2	2820510H1	2657	2994
16	252964.2	3620806H1	596	894
16	252964.2	450871R6	789	1191
16	252964.2	2367753T6	820	1282
16	252964.2	633611H1	831	1087
16	252964.2	2791431H1	860	1136
16	252964.2	3233115H1	649	894
16	252964.2	746957H1	919	1176
16	252964.2	1839028H1	1018	1185
16	252964.2	g4394691	686	1065
16	252964.2	1838057H1	1018	1320
16	252964.2	g1993698	1033	1347
16	252964.2	4292134H1	1058	1315
16	252964.2	g869109	1093	1386
16	252964.2	g792911	1095	1358
16	252964.2	g2269330	700	1066
16	252964.2	g2444529	1098	1482
16	252964.2	452142H1	1120	1366
16	252964.2	4239190H1	740	1007
16	252964.2	4046046H1	1134	1403
16	252964.2	1993076F6	1136	1449
16	252964.2	1993076H1	1136	1292

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
16	252964.2	945488R6	1173	1668
16	252964.2	945488H1	1172	1463
16	252964.2	5434372H1	1176	1384
16	252964.2	2701918H1	1267	1540
16	252964.2	997219H1	1312	1504
16	252964.2	997219R2	1312	1842
16	252964.2	596014H1	1363	1597
16	252964.2	160577H1	1398	1597
16	252964.2	g573332	1426	1787
16	252964.2	g677613	1426	1779
16	252964.2	g1998633	783	1161
16	252964.2	5193886H1	1448	1687
16	252964.2	g2052933	1483	1589
16	252964.2	5192721H1	1589	1859
16	252964.2	g2218358	1592	1916
16	252964.2	4108761H1	1608	1895
16	252964.2	g1165576	1619	1872
16	252964.2	3285590H1	1701	1945
16	252964.2	5713371H1	1715	2000
16	252964.2	1877915H1	1767	1928
16	252964.2	450871H1	789	1015
16	252964.2	1877915F6	1767	2150
16	252964.2	5615447H1	1	281
16	252964.2	1871935F6	8	479
16	252964.2	1871935H1	8	263
16	252964.2	1871835H1	8	247
16	252964.2	2787027H1	101	429
16	252964.2	3770821H1	319	618
16	252964.2	5291758H1	346	547
16	252964.2	g1545134	439	843
16	252964.2	g1063095	439	811
16	252964.2	g272283	469	804
16	252964.2	2670348T6	493	1024
16	252964.2	1871935T6	528	1019
16	252964.2	2367753F6	563	974
16	252964.2	2367753H1	563	788
17	267153.7	2580428F6	1	424
17	267153.7	5780256H1	7	197
17	267153.7	1927531H1	1	104
17	267153.7	5542321H1	1	86
17	267153.7	2580428H1	1	211
17	267153.7	g2033888	656	925
17	267153.7	g2033889	656	842
17	267153.7	g2034039	656	1001
17	267153.7	g2034000	656	969
17	267153.7	g2033922	656	925
17	267153.7	556169H1	663	808
17	267153.7	556169R6	663	1220
17	267153.7	553115H1	663	885
17	267153.7	986072H1	693	802

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
17	267153.7	4180466H1	1166	1393
17	267153.7	4180466F6	1166	1456
17	267153.7	1416069H1	1351	1620
17	267153.7	3047572F6	1402	1874
17	267153.7	3047572H1	1403	1708
17	267153.7	5422118H1	1463	1711
17	267153.7	3241209H1	1499	1736
17	267153.7	3577671H1	18	193
17	267153.7	5636615H1	18	164
17	267153.7	5322669H1	29	285
17	267153.7	5321675H1	29	298
17	267153.7	3227664F6	31	402
17	267153.7	3406115H1	31	290
17	267153.7	3799455H1	31	255
17	267153.7	3227664H1	33	322
17	267153.7	3146326H1	35	333
17	267153.7	4760440H1	45	149
17	267153.7	3378285H1	54	286
17	267153.7	3799580H1	69	370
17	267153.7	3366109H1	109	317
17	267153.7	g2229557	110	441
17	267153.7	6078201H1	381	715
17	267153.7	g923914	419	670
17	267153.7	g274698	464	842
17	267153.7	g781645	644	877
18	331244.6	g2037184	293	666
18	331244.6	3703079H1	295	604
18	331244.6	4355792H1	298	664
18	331244.6	5205414H2	299	581
18	331244.6	5662744H1	307	557
18	331244.6	1818166H1	312	602
18	331244.6	1428020F6	313	785
18	331244.6	2867856H1	314	547
18	331244.6	2534359H2	315	500
18	331244.6	2852946H1	315	629
18	331244.6	4909270H1	315	593
18	331244.6	5895948H1	321	625
18	331244.6	5902265H1	322	603
18	331244.6	g1970235	332	646
18	331244.6	4700222H1	335	620
18	331244.6	3367010H1	336	601
18	331244.6	g2103204	351	812
18	331244.6	3929559H1	352	666
18	331244.6	036372H1	353	586
18	331244.6	058809H1	358	537
18	331244.6	2726788H1	358	614
18	331244.6	g1110314	362	671
18	331244.6	351602H1	363	604
18	331244.6	1352253H1	1	254
18	331244.6	1352253F1	1	575

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
18	331244.6	1352253F6	1	465
18	331244.6	2600773H1	363	680
18	331244.6	4718931H1	42	313
18	331244.6	2656868H1	363	576
18	331244.6	2605832H1	363	595
18	331244.6	3436228H1	363	598
18	331244.6	5118860H1	364	653
18	331244.6	2024732H1	366	624
18	331244.6	4371963H1	371	641
18	331244.6	100587H1	43	245
18	331244.6	1867334H1	49	224
18	331244.6	3597304H1	48	367
18	331244.6	2451902H1	50	289
18	331244.6	2738608H1	50	294
18	331244.6	g771569	51	434
18	331244.6	g1803076	53	131
18	331244.6	4718914H1	61	332
18	331244.6	4719022H1	62	170
18	331244.6	4373837H1	371	652
18	331244.6	043783H1	381	689
18	331244.6	g1678313	381	800
18	331244.6	841019H1	387	650
18	331244.6	841019R1	387	1002
18	331244.6	1995102R6	400	826
18	331244.6	1995102H1	400	695
18	331244.6	3855550H1	404	726
18	331244.6	g766559	115	361
18	331244.6	g2034844	121	481
18	331244.6	g880214	204	609
18	331244.6	g751349	253	587
18	331244.6	535267H1	280	511
18	331244.6	1428020H1	282	477
18	331244.6	1427648H1	282	560
18	331244.6	3450701H1	286	545
18	331244.6	1718398H1	455	670
18	331244.6	3025271H1	478	761
18	331244.6	3057108H1	481	665
18	331244.6	4773103H1	518	829
18	331244.6	942862R1	528	983
18	331244.6	942862H1	528	778
18	331244.6	1302039H1	552	849
18	331244.6	4981303H1	560	837
18	331244.6	2101923H1	645	907
18	331244.6	3972632H1	696	975
18	331244.6	2327160H1	712	967
18	331244.6	2232654H1	731	975
18	331244.6	3818861H1	732	1029
18	331244.6	1609537H1	732	933
18	331244.6	1609517H1	732	920
18	331244.6	4710176H1	734	896

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
18	331244.6	4710284H1	734	1011
18	331244.6	g2595082	755	945
18	331244.6	4049284H1	772	1069
18	331244.6	1538495H1	798	999
18	331244.6	1228870H1	844	1094
18	331244.6	2628877H1	861	1098
18	331244.6	4995618H1	875	1144
18	331244.6	1995102T6	877	1530
18	331244.6	2043991H1	884	1126
18	331244.6	3516482H1	915	1177
18	331244.6	1996374T6	922	1532
18	331244.6	1996374R6	939	1439
18	331244.6	1996374H1	939	1206
18	331244.6	1549444H1	939	1164
18	331244.6	4324734H1	945	1185
18	331244.6	336097H1	1003	1259
18	331244.6	g2017702	1007	1387
18	331244.6	2425889H1	1035	1298
18	331244.6	3411191H1	1036	1202
18	331244.6	3078834H1	1103	1417
18	331244.6	480272H1	1113	1369
18	331244.6	g2103137	1128	1585
18	331244.6	g712162	1138	1574
18	331244.6	g4525329	1137	1571
18	331244.6	549094H1	1146	1442
18	331244.6	2579048H2	1154	1442
18	331244.6	1414589F6	1177	1583
18	331244.6	1414589H1	1177	1439
18	331244.6	g3841570	1187	1575
18	331244.6	g794847	1206	1589
18	331244.6	4640449H1	1219	1507
18	331244.6	g3840885	1222	1571
18	331244.6	g819967	1280	1581
18	331244.6	g751350	1272	1573
18	331244.6	4367801H1	1281	1528
18	331244.6	g519529	1293	1571
18	331244.6	g618115	1361	1575
19	335484.1	2626409H1	2774	3005
19	335484.1	2626409F6	2774	3290
19	335484.1	2626025H1	2774	3030
19	335484.1	1418291H1	2841	3077
19	335484.1	g2397783	2874	3259
19	335484.1	2746883H1	2914	3175
19	335484.1	2626409T6	3031	3264
19	335484.1	g4270950	3127	3574
19	335484.1	g2899058	3132	3575
19	335484.1	2521894F6	148	661
19	335484.1	2521894H1	148	407
19	335484.1	5538378H1	264	471
19	335484.1	3465291H1	316	642

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
19	335484.1	g1623573	318	650
19	335484.1	g715634	78	309
19	335484.1	5386328H1	330	594
19	335484.1	g764148	79	353
19	335484.1	g2012728	369	603
19	335484.1	5854480H1	414	711
19	335484.1	2671282F6	1138	1680
19	335484.1	3115951F6	1497	1895
19	335484.1	3115951H1	1498	1773
19	335484.1	g570994	1528	1910
19	335484.1	g672096	1529	1865
19	335484.1	g677051	1529	1830
19	335484.1	g781962	1542	1799
19	335484.1	g668551	1542	1803
19	335484.1	4010291H1	1563	1839
19	335484.1	2401422H1	1728	1969
19	335484.1	3695649H1	2034	2334
19	335484.1	g3240345	1869	2245
19	335484.1	3293772F6	2059	2440
19	335484.1	3293772H1	2059	2332
19	335484.1	116622H1	2085	2321
19	335484.1	116622R1	2085	2558
19	335484.1	5171287H1	2170	2380
19	335484.1	5175487H1	2170	2442
19	335484.1	2671282T6	2172	2748
19	335484.1	5098225H1	419	697
19	335484.1	5677977H1	969	1230
19	335484.1	g1626824	970	1275
19	335484.1	5098225F6	419	691
19	335484.1	5098225T6	432	1048
19	335484.1	g2694430	439	905
19	335484.1	g2357857	995	1365
19	335484.1	g1289722	522	916
19	335484.1	5645168H1	633	884
19	335484.1	g715547	802	902
19	335484.1	g3239654	843	1073
19	335484.1	1978183H1	1014	1276
19	335484.1	5834795H1	1067	1337
19	335484.1	2671282H1	1138	1379
19	335484.1	g1321140	1	418
19	335484.1	3448433H1	1	238
19	335484.1	4380511H1	16	285
19	335484.1	3576080H1	40	293
19	335484.1	3463823H1	64	314
19	335484.1	3115951T6	2174	2742
19	335484.1	116622F1	2216	2785
19	335484.1	4172444H1	2216	2512
19	335484.1	3721925H1	2298	2603
19	335484.1	g2902979	2336	2799
19	335484.1	g822642	2488	2802

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
19	335484.1	g562662	2502	2785
19	335484.1	2936989H1	2520	2782
19	335484.1	g671386	2547	2785
19	335484.1	g646350	2577	2785
19	335484.1	g645116	2579	2785
19	335484.1	g2805833	2664	2797
19	335484.1	3293772T6	2748	3218
20	337489.2	4945764H1	1	263
20	337489.2	g1985316	1	217
20	337489.2	3247865H1	11	317
20	337489.2	4180529H1	15	112
20	337489.2	385371H1	166	429
20	337489.2	g1624554	389	725
20	337489.2	3078832F6	392	796
20	337489.2	3078832H1	392	697
20	337489.2	3294510H1	650	824
20	337489.2	g395753	669	1006
20	337489.2	g2184364	816	1265
20	337489.2	6075740H1	885	1174
20	337489.2	6075772H1	903	1168
20	337489.2	3078832T6	1009	1457
21	359574.5	g2398327	1	343
21	359574.5	g2629710	1	421
21	359574.5	3338142H1	1	233
21	359574.5	3685831H1	30	171
21	359574.5	2993588H1	40	306
21	359574.5	1906768F6	41	453
21	359574.5	1906768H1	41	118
21	359574.5	3172672H1	46	229
21	359574.5	3436865H1	47	289
21	359574.5	1818045H1	47	342
21	359574.5	g1781952	66	480
21	359574.5	3982668H1	72	264
21	359574.5	1672722H1	75	282
21	359574.5	3036287H1	107	372
21	359574.5	g1578363	103	345
21	359574.5	g827499	106	477
21	359574.5	4054942H1	123	423
21	359574.5	3340967H1	132	397
21	359574.5	3433495H1	132	218
21	359574.5	g1735769	158	554
21	359574.5	1390555H1	188	376
21	359574.5	1390555F6	188	565
21	359574.5	987088H1	190	476
21	359574.5	5850596H1	204	395
21	359574.5	2204622H1	326	591
21	359574.5	2204622F6	326	853
21	359574.5	g1961866	385	793
21	359574.5	1967881H1	396	690
21	359574.5	5059229H1	397	672

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SEQ ID NO:	Template ID	Component ID	Start	Stop
21	359574.5	3199313H1	463	561
21	359574.5	1006996H1	511	748
21	359574.5	3054689H1	547	838
21	359574.5	1965560H1	692	968
21	359574.5	5544945H1	716	949
21	359574.5	3376272H1	741	918
21	359574.5	g899846	882	1212
21	359574.5	g389140	910	1319
21	359574.5	g616300	914	1190
21	359574.5	5636083H1	920	1214
21	359574.5	g3769768	924	1005
21	359574.5	3804657H1	943	1272
21	359574.5	1347412H1	967	1224
21	359574.5	270746H1	974	1326
21	359574.5	493004H1	977	1377
21	359574.5	4915149H1	979	1259
21	359574.5	3289817H1	1044	1181
21	359574.5	747411R1	1057	1741
21	359574.5	747411H1	1057	1300
21	359574.5	1902775F6	1102	1593
21	359574.5	1902775H1	1102	1380
21	359574.5	3331792H1	1170	1463
21	359574.5	4787713H1	1231	1489
21	359574.5	5101264H1	1240	1501
21	359574.5	g1578064	2292	2727
21	359574.5	045454H1	2294	2533
21	359574.5	g2063879	2309	2770
21	359574.5	g848870	2314	2662
21	359574.5	g848899	2314	2632
21	359574.5	4731068H1	2312	2586
21	359574.5	g848913	2322	2712
21	359574.5	3494155H1	2327	2593
21	359574.5	4180013T6	2338	2792
21	359574.5	413579H1	2342	2590
21	359574.5	415164H1	2342	2589
21	359574.5	2905578T6	2345	2775
21	359574.5	1841356T6	2347	2748
21	359574.5	1713137T6	2345	2762
21	359574.5	g3109931	2355	2819
21	359574.5	g2705028	2359	2817
21	359574.5	g2752959	2359	2815
21	359574.5	g3752541	2360	2815
21	359574.5	g1578272	2370	2817
21	359574.5	g1941192	2370	2820
21	359574.5	g2001627	2385	2815
21	359574.5	g4114546	2380	2815
21	359574.5	3866784H1	2380	2664
21	359574.5	981891H1	2383	2661
21	359574.5	1500830T6	2387	2773
21	359574.5	g2883824	2389	2818

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
21	359574.5	g1741113	2392	2814
21	359574.5	g1815396	2394	2816
21	359574.5	g3921165	2402	2815
21	359574.5	g3277950	2404	2821
21	359574.5	g3777806	2405	2780
21	359574.5	g4389617	2405	2815
21	359574.5	g4394654	2408	2816
21	359574.5	5161988H1	2412	2686
21	359574.5	g1940064	2414	2820
21	359574.5	g3190460	2418	2815
21	359574.5	g2159890	2419	2819
21	359574.5	g848914	2422	2821
21	359574.5	g3280154	2423	2818
21	359574.5	g2063754	2428	2816
21	359574.5	g1010758	2429	2828
21	359574.5	744138R1	2433	2815
21	359574.5	g1940045	2433	2820
21	359574.5	744138H1	2433	2681
21	359574.5	985588R1	2441	2815
21	359574.5	985588T1	2441	2772
21	359574.5	985588H1	2441	2703
21	359574.5	g848871	2450	2815
21	359574.5	g848900	2461	2792
21	359574.5	g519499	2467	2815
21	359574.5	g3801239	2477	2818
21	359574.5	g890240	2479	2795
21	359574.5	g3245088	2483	2820
21	359574.5	g4308927	2485	2815
21	359574.5	g712131	2490	2816
21	359574.5	676177H1	2497	2753
21	359574.5	674403H1	2497	2775
21	359574.5	677641H1	2497	2780
21	359574.5	g2955368	2508	2823
21	359574.5	1306109F6	2513	2815
21	359574.5	1306109T6	2515	2787
21	359574.5	g2985090	2523	2815
21	359574.5	4509027H1	2523	2796
21	359574.5	3482667H1	2525	2773
21	359574.5	g1781898	2533	2819
21	359574.5	g3843043	2548	2816
21	359574.5	g4088596	2553	2815
21	359574.5	3203278H1	2562	2772
21	359574.5	g3862263	2579	2818
21	359574.5	g2783892	2589	2813
21	359574.5	g1241936	2605	2815
21	359574.5	g2968846	2752	2815
21	359574.5	121182H1	1243	1366
21	359574.5	3929693H1	1258	1451
21	359574.5	3929728H1	1258	1553
21	359574.5	3929244H1	1258	1542

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
21	359574.5	2583640H1	1299	1548
21	359574.5	3720446H1	1302	1550
21	359574.5	701602H1	1304	1583
21	359574.5	1533449H1	1349	1556
21	359574.5	3778291H1	1382	1674
21	359574.5	3444913H1	1400	1687
21	359574.5	3444961H1	1400	1679
21	359574.5	g958359	1426	1664
21	359574.5	4754535H1	1428	1647
21	359574.5	5413181H1	1438	1592
21	359574.5	4198550H1	1443	1721
21	359574.5	2310430H1	1479	1764
21	359574.5	4027760H1	1489	1759
21	359574.5	4016122H1	1535	1836
21	359574.5	g869879	1540	1599
21	359574.5	3442527H1	1567	1817
21	359574.5	4885815H1	1582	1849
21	359574.5	g1275597	1609	1963
21	359574.5	4695180H1	1619	1885
21	359574.5	4695474H1	1620	1894
21	359574.5	g901597	1664	2045
21	359574.5	1007934H1	1689	2008
21	359574.5	4822784H1	1699	1898
21	359574.5	533880H1	1726	2009
21	359574.5	5273871H1	1733	1997
21	359574.5	1822559H1	1733	1991
21	359574.5	4771544H1	1736	2019
21	359574.5	957505H1	1739	1874
21	359574.5	1419462H1	1764	2012
21	359574.5	1419438H1	1764	2023
21	359574.5	5377747H1	1767	2042
21	359574.5	3090935H1	1767	2048
21	359574.5	2578414H1	1767	2041
21	359574.5	3055886H1	1777	1996
21	359574.5	4307872H1	1798	1913
21	359574.5	5888134H1	1809	2090
21	359574.5	5881810H1	1809	2029
21	359574.5	5881543H1	1809	2092
21	359574.5	5885336H1	1809	2092
21	359574.5	1756055H1	1832	2078
21	359574.5	1756070R6	1832	2190
21	359574.5	669694H1	1851	2139
21	359574.5	2819291H1	1851	2162
21	359574.5	669348H1	1851	2136
21	359574.5	4376341H1	1872	2139
21	359574.5	g1815577	1876	2377
21	359574.5	5272067H1	1880	2149
21	359574.5	1713137F6	1887	2285
21	359574.5	1713137H1	1889	2114
21	359574.5	3457357H1	1894	2156

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
21	359574.5	173730H1	1910	2114
21	359574.5	5897973H1	1917	2178
21	359574.5	5902784H1	1917	2216
21	359574.5	359622H1	1919	2162
21	359574.5	960614R1	1945	2549
21	359574.5	960614H1	1945	2236
21	359574.5	1811654F6	1965	2504
21	359574.5	1811654H1	1965	2193
21	359574.5	2244848H1	2044	2311
21	359574.5	108439H1	2050	2312
21	359574.5	5055320H1	2113	2403
21	359574.5	4168527H1	2115	2416
21	359574.5	993418H1	2116	2352
21	359574.5	4175578H1	2134	2428
21	359574.5	3121162H1	2142	2427
21	359574.5	1663986H1	2147	2381
21	359574.5	1756070T6	2173	2775
21	359574.5	2744396H1	2182	2464
21	359574.5	5052765H1	2187	2452
21	359574.5	2697857T6	2207	2773
21	359574.5	2597236H1	2219	2487
21	359574.5	g890239	2240	2516
21	359574.5	g944471	2245	2444
21	359574.5	g1940156	2246	2668
21	359574.5	g1940137	2246	2687
21	359574.5	345599H1	2246	2484
21	359574.5	g1941570	2246	2712
21	359574.5	345599R1	2246	2815
21	359574.5	345599T6	2246	2773
21	359574.5	345599R6	2246	2711
21	359574.5	g944601	2257	2495
21	359574.5	3376272T6	2263	2783
21	359574.5	2875472H1	2286	2576
21	359574.5	5263385H1	2291	2476
21	359574.5	5263484H1	2291	2570
22	360645.5	3292408H1	459	712
22	360645.5	3316570H1	482	745
22	360645.5	2419778H1	627	854
22	360645.5	2069602F6	718	1133
22	360645.5	2069602H1	718	1005
22	360645.5	g1989917	895	1120
22	360645.5	2741388H1	919	1046
22	360645.5	3870739H1	928	1208
22	360645.5	g793668	936	1225
22	360645.5	4328833H1	949	1209
22	360645.5	g810427	1514	1829
22	360645.5	3337383H1	1563	1830
22	360645.5	4544819H1	1572	1859
22	360645.5	755269H1	1493	1731
22	360645.5	5674837H1	1503	1781

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
22	360645.5	4370282H1	1672	1936
22	360645.5	5622513H1	1718	1985
22	360645.5	1655614T6	1751	2297
22	360645.5	3943544H1	1865	2133
22	360645.5	5114825H1	2045	2300
22	360645.5	4003719H1	58	111
22	360645.5	3246721H1	68	332
22	360645.5	g4307092	100	560
22	360645.5	1532088H1	108	298
22	360645.5	1532088F6	108	498
22	360645.5	5016056H1	116	341
22	360645.5	5730961H1	957	1236
22	360645.5	g928494	968	1138
22	360645.5	3945858H1	988	1262
22	360645.5	2757979H1	1000	1280
22	360645.5	853610H1	1008	1266
22	360645.5	858390H1	1008	1228
22	360645.5	g3932189	137	556
22	360645.5	4862779H1	142	426
22	360645.5	4988340H1	237	514
22	360645.5	3460296H1	131	357
22	360645.5	750638H1	237	461
22	360645.5	4141768H1	386	657
22	360645.5	2607858T6	2162	2289
22	360645.5	492034H1	1	112
22	360645.5	3433917H1	1	243
22	360645.5	928400R6	9	371
22	360645.5	2607858H1	29	288
22	360645.5	2607858F6	29	372
22	360645.5	3111874H1	33	168
22	360645.5	3286166H2	33	137
22	360645.5	3346552H1	33	146
22	360645.5	928400H1	35	296
22	360645.5	3392281H1	40	321
22	360645.5	2562696H1	1447	1749
22	360645.5	2562696R6	1447	1930
22	360645.5	1655614F6	1468	2026
22	360645.5	1655614H1	1468	1602
22	360645.5	3780371H1	1479	1725
22	360645.5	3674986H1	1482	1626
22	360645.5	4294260H1	1490	1738
22	360645.5	5424404H1	1492	1695
22	360645.5	4118032H1	1010	1193
22	360645.5	3484111H1	1011	1329
22	360645.5	3749318H1	1089	1394
22	360645.5	g2139442	1114	1465
22	360645.5	g813345	1194	1462
22	360645.5	2185958F6	1196	1667
22	360645.5	2185958H1	1196	1475
22	360645.5	5471220H1	1268	1469

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
22	360645.5	4907477H1	1282	1514
22	360645.5	4931374H1	1291	1569
22	360645.5	5554128H1	1307	1579
22	360645.5	3852884H1	1316	1599
22	360645.5	2605946H1	1430	1682
22	360645.5	2605946F6	1430	1850
23	404145.7	1226940T6	2019	2668
23	404145.7	1384452H1	2040	2300
23	404145.7	g2849417	2162	2715
23	404145.7	g823503	2173	2683
23	404145.7	3406347H1	2172	2452
23	404145.7	999039T6	2184	2670
23	404145.7	1540442H1	2182	2421
23	404145.7	g982396	2199	2455
23	404145.7	g712667	2199	2485
23	404145.7	g1981065	2198	2524
23	404145.7	515954H1	2206	2479
23	404145.7	1422474H1	2212	2431
23	404145.7	1422482H1	2212	2425
23	404145.7	2059115H1	2218	2298
23	404145.7	5675554H1	2212	2487
23	404145.7	4296263H1	2231	2519
23	404145.7	g3958774	2305	2714
23	404145.7	g3848380	2304	2711
23	404145.7	g2254693	2310	2711
23	404145.7	3461604H1	1327	1395
23	404145.7	4695473H1	1331	1607
23	404145.7	4874584H1	1350	1628
23	404145.7	4787505H1	1176	1448
23	404145.7	255532H1	1351	1453
23	404145.7	2634636H1	1355	1622
23	404145.7	g832545	1379	1449
23	404145.7	4115082H1	1181	1460
23	404145.7	3782056H1	1386	1713
23	404145.7	g706330	1182	1437
23	404145.7	g2156249	1209	1450
23	404145.7	g567479	1209	1446
23	404145.7	g4327617	1215	1446
23	404145.7	3453995H1	1439	1718
23	404145.7	5085837H1	1440	1592
23	404145.7	g868972	1221	1465
23	404145.7	1623692H1	1263	1452
23	404145.7	388050H1	1276	1448
23	404145.7	494624H1	1454	1689
23	404145.7	1209507H1	1458	1685
23	404145.7	g573709	1284	1576
23	404145.7	g872902	1297	1625
23	404145.7	g2156298	1300	1447
23	404145.7	1209507R1	1458	2035
23	404145.7	5849810H1	1322	1615

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
23	404145.7	2716195H1	1460	1573
23	404145.7	4854635H1	1326	1576
23	404145.7	3875565H1	1477	1783
23	404145.7	4764440H1	1487	1750
23	404145.7	4764803H1	1487	1776
23	404145.7	504658H1	1492	1716
23	404145.7	2245901H1	1492	1745
23	404145.7	1554072H1	1522	1749
23	404145.7	4306748H1	1522	1648
23	404145.7	681646H1	1599	1730
23	404145.7	3397784H1	1660	1877
23	404145.7	4775418H1	1709	1991
23	404145.7	4320445H1	1743	2009
23	404145.7	5516752H1	1748	1890
23	404145.7	g1300713	1768	1930
23	404145.7	g2022370	1777	2020
23	404145.7	3573326H1	1779	2074
23	404145.7	2365670F6	983	1446
23	404145.7	4080981H1	990	1144
23	404145.7	g3694292	989	1450
23	404145.7	2365670H1	983	1211
23	404145.7	g4187437	990	1449
23	404145.7	1979701T6	989	1407
23	404145.7	g1941609	991	1450
23	404145.7	1979701H1	989	1100
23	404145.7	g2401947	999	1447
23	404145.7	g4175914	1010	1446
23	404145.7	g4186516	1012	1446
23	404145.7	5903586H1	243	372
23	404145.7	5895277H1	243	542
23	404145.7	713562H1	264	456
23	404145.7	1859327H1	283	553
23	404145.7	g2240756	298	640
23	404145.7	3802569H1	377	675
23	404145.7	3801769H1	376	685
23	404145.7	4160262H1	403	663
23	404145.7	3386012H1	417	669
23	404145.7	3672136H1	430	701
23	404145.7	3225464H1	446	551
23	404145.7	g1376475	496	934
23	404145.7	4125118H1	555	694
23	404145.7	2957060H1	594	885
23	404145.7	3615068H1	595	900
23	404145.7	5290436H1	596	868
23	404145.7	3035696F6	601	1194
23	404145.7	3035696H1	601	897
23	404145.7	2538441H1	650	866
23	404145.7	1927342H1	658	924
23	404145.7	3760928H1	664	986
23	404145.7	1927342T6	753	1404

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
23	404145.7	4895377H1	762	1007
23	404145.7	2956245H1	792	1071
23	404145.7	3343627H1	800	1065
23	404145.7	3535153H1	804	1024
23	404145.7	g2558289	815	1224
23	404145.7	231872F1	894	1446
23	404145.7	g2080439	930	1431
23	404145.7	866856R1	953	1577
23	404145.7	866856H1	954	1267
23	404145.7	g3230192	957	1458
23	404145.7	g4076020	965	1450
23	404145.7	g2080362	964	1449
23	404145.7	2775965H1	973	1254
23	404145.7	3729250H1	973	1309
23	404145.7	g4453632	976	1446
23	404145.7	g4137344	977	1446
23	404145.7	2365670T6	976	1402
23	404145.7	2208265H1	981	1247
23	404145.7	5067178H1	973	1228
23	404145.7	2258456H1	983	1254
23	404145.7	1809649F6	1	446
23	404145.7	1809649H1	1	236
23	404145.7	g868971	18	380
23	404145.7	g766530	18	261
23	404145.7	3753077H1	69	380
23	404145.7	3212973H1	103	385
23	404145.7	3504947H1	110	414
23	404145.7	5287655H1	184	359
23	404145.7	929914R1	220	782
23	404145.7	929914H1	220	443
23	404145.7	4615617H1	1909	2168
23	404145.7	1304785H1	1912	2125
23	404145.7	5832281H1	1844	2103
23	404145.7	809035H1	1989	2155
23	404145.7	1793716R6	1996	2294
23	404145.7	1793716H1	1996	2260
23	404145.7	2562614H1	2007	2225
23	404145.7	2952424H1	1876	2161
23	404145.7	3282561H1	2012	2272
23	404145.7	2955893H1	1876	2137
23	404145.7	1226940R6	2014	2233
23	404145.7	1226940H1	2014	2270
23	404145.7	674047H1	2017	2299
23	404145.7	675500H1	2017	2292
23	404145.7	g982397	2454	2704
23	404145.7	g3003541	2472	2708
23	404145.7	g566129	2520	2706
23	404145.7	g2022554	2549	2711
23	404145.7	808819H1	2625	2711
23	404145.7	1719821H1	2323	2479

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
23	404145.7	g3849700	2323	2720
23	404145.7	1652087T6	2323	2672
23	404145.7	1719821F6	2323	2673
23	404145.7	914198H1	2330	2630
23	404145.7	5779135H1	2329	2596
23	404145.7	g3895240	2356	2712
23	404145.7	3410322H1	2369	2613
23	404145.7	g2254107	2370	2712
23	404145.7	3035696T6	2372	2673
23	404145.7	g872903	2394	2719
23	404145.7	g3899723	2414	2712
23	404145.7	g1754350	2415	2704
23	404145.7	g4451440	2429	2712
23	404145.7	3105351H1	2437	2704
23	404145.7	g2278302	1017	1445
23	404145.7	g4264482	1018	1446
23	404145.7	g2167436	1016	1446
23	404145.7	g2569624	1016	1446
23	404145.7	g3785423	1022	1446
23	404145.7	g3446161	1023	1446
23	404145.7	g3757074	1031	1453
23	404145.7	4894986H1	1036	1338
23	404145.7	g1332103	1031	1454
23	404145.7	g4108387	1032	1446
23	404145.7	g674079	1041	1448
23	404145.7	4605744H1	1063	1335
23	404145.7	4605666H1	1063	1339
23	404145.7	3270540H1	1068	1326
23	404145.7	1624105H1	1083	1264
23	404145.7	g1376427	1088	1447
23	404145.7	g2809882	1103	1446
23	404145.7	1339468H1	1128	1390
23	404145.7	1340790H1	1128	1360
23	404145.7	3272590H1	1128	1397
23	404145.7	4583083H1	1135	1407
23	404145.7	g4077930	1135	1453
23	404145.7	g817212	1153	1450
24	480119.1	2352304H1	739	946
24	480119.1	3758378H1	1117	1297
24	480119.1	2094276H1	900	1179
24	480119.1	3280967H1	806	1056
24	480119.1	342432H1	940	1165
24	480119.1	2082987H1	906	1175
24	480119.1	5499718H1	1123	1223
24	480119.1	3374480H1	972	1247
24	480119.1	2715270H1	734	1001
24	480119.1	670230H1	802	1052
24	480119.1	2860379H1	964	1231
24	480119.1	3792137H1	848	1151
24	480119.1	2860343H1	964	1210

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
24	480119.1	997621H1	959	1209
24	480119.1	3055163H1	949	1191
24	480119.1	998148H1	1	280
24	480119.1	1908860F6	121	498
24	480119.1	1908860H1	121	226
24	480119.1	5639607H1	455	586
24	480119.1	3003224H1	516	790
24	480119.1	1229820H1	711	819
24	480119.1	g4307656	724	1062
24	480119.1	g3336553	744	1112
24	480119.1	3153981H1	806	1078
24	480119.1	669605H1	807	1071
24	480119.1	3376935H1	849	1097
24	480119.1	1636772F6	855	1316
24	480119.1	2579416H1	863	1102
24	480119.1	668857H1	967	1069
24	480119.1	4252513H1	968	1126
24	480119.1	1636772T6	1135	1336
24	480119.1	4066993H1	757	1016
24	480119.1	1945549H1	591	817
24	480119.1	1672355H1	994	1205
25	480951.5	3507776H1	1269	1599
25	480951.5	4822022H1	1279	1597
25	480951.5	g1980640	1281	1642
25	480951.5	g1227074	1282	1672
25	480951.5	635081H1	1281	1577
25	480951.5	g2525370	1282	1667
25	480951.5	g2224141	1287	1673
25	480951.5	633976H1	1295	1566
25	480951.5	g1813260	1304	1683
25	480951.5	g3673968	1303	1667
25	480951.5	g1141351	1306	1674
25	480951.5	5733042H1	1306	1556
25	480951.5	4115350H1	1306	1589
25	480951.5	500639H1	1307	1589
25	480951.5	g3891298	1311	1670
25	480951.5	g1718633	1315	1675
25	480951.5	g1401801	1316	1669
25	480951.5	g989254	1317	1682
25	480951.5	g2070629	1318	1684
25	480951.5	g698987	1325	1714
25	480951.5	g698871	1325	1642
25	480951.5	g1319182	1325	1781
25	480951.5	g2898680	1325	1767
25	480951.5	g2806772	1327	1547
25	480951.5	3359017H1	1249	1564
25	480951.5	g4089542	1255	1669
25	480951.5	765793H1	1260	1536
25	480951.5	3492863H1	1327	1629
25	480951.5	g2779619	1327	1667

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
25	480951.5	686048H1	1327	1620
25	480951.5	g2617638	1261	1655
25	480951.5	g3677064	1263	1673
25	480951.5	3398923H1	1263	1523
25	480951.5	4729307H1	1267	1545
25	480951.5	5217308H1	1261	1532
25	480951.5	1221016H1	1328	1583
25	480951.5	2447883H1	1338	1603
25	480951.5	g1102813	1338	1697
25	480951.5	g2669446	1351	1670
25	480951.5	2048112H1	1369	1667
25	480951.5	2790672H1	1372	1695
25	480951.5	2234076H1	1375	1672
25	480951.5	3862273H1	1376	1622
25	480951.5	4247109H1	1377	1675
25	480951.5	4880414H1	1378	1671
25	480951.5	g1670201	1384	1667
25	480951.5	5077294H1	1391	1667
25	480951.5	g782958	1396	1672
25	480951.5	3142143H1	1393	1693
25	480951.5	069655H1	1400	1600
25	480951.5	g4089195	1401	1676
25	480951.5	2360852H1	1405	1684
25	480951.5	1220650H1	1416	1672
25	480951.5	g981974	1416	1648
25	480951.5	g2035110	1427	1667
25	480951.5	497474H1	1433	1647
25	480951.5	g2751121	1433	1670
25	480951.5	g1998201	1463	1848
25	480951.5	g1996178	1463	1769
25	480951.5	2284547H1	1463	1725
25	480951.5	6013816H1	1488	1667
25	480951.5	g1067287	1496	1852
25	480951.5	g1401911	776	1312
25	480951.5	2423201H1	2372	2629
25	480951.5	g884922	2375	2737
25	480951.5	122603H1	2383	2588
25	480951.5	114097F1	2383	2736
25	480951.5	g1547877	2387	2736
25	480951.5	533580H1	2387	2655
25	480951.5	g1625895	2388	2744
25	480951.5	g892913	2389	2745
25	480951.5	4760035H1	2411	2725
25	480951.5	2029001H1	2411	2700
25	480951.5	5978765H1	2410	2729
25	480951.5	g3076031	2412	2739
25	480951.5	1288402H1	2417	2690
25	480951.5	g1240606	2425	2736
25	480951.5	3729607H1	2426	2723
25	480951.5	g1740278	2437	2742

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
25	480951.5	g1690726	2453	2737
25	480951.5	g1070677	2455	2736
25	480951.5	g1505473	2455	2736
25	480951.5	565823H1	2457	2695
25	480951.5	564237H1	2457	2719
25	480951.5	g3784617	2458	2739
25	480951.5	g4292869	2458	2723
25	480951.5	501474H1	2457	2680
25	480951.5	532322H1	2463	2744
25	480951.5	g1114717	2474	2739
25	480951.5	g990510	2478	2730
25	480951.5	g1271273	2490	2741
25	480951.5	g796298	2493	2745
25	480951.5	g4137432	2508	2737
25	480951.5	2907345H1	2514	2736
25	480951.5	g4389704	2523	2736
25	480951.5	865791T1	2543	3032
25	480951.5	865791H1	2543	2787
25	480951.5	2042379H1	2589	2733
25	480951.5	2412014H1	2608	2736
25	480951.5	3934970H1	2609	2742
25	480951.5	g4532798	2613	2736
25	480951.5	g3919950	2618	2736
25	480951.5	2108271H1	2638	2736
25	480951.5	5921804H1	2644	2736
25	480951.5	4020876H1	2665	2736
25	480951.5	g2070432	724	1019
25	480951.5	3579019H1	740	1053
25	480951.5	376204H1	747	1026
25	480951.5	1672679H1	751	878
25	480951.5	2839053H1	753	1032
25	480951.5	4192530H1	763	1028
25	480951.5	5283432H1	763	1029
25	480951.5	4575886H1	774	1052
25	480951.5	3750596H1	1	163
25	480951.5	g2056998	1	224
25	480951.5	2613688H1	9	250
25	480951.5	3541978H1	19	226
25	480951.5	3395818H1	39	330
25	480951.5	3395687H1	38	285
25	480951.5	3117868H1	70	261
25	480951.5	g2057109	161	443
25	480951.5	g2229512	237	678
25	480951.5	5542378H1	251	438
25	480951.5	3451601H1	298	471
25	480951.5	3243270H1	308	566
25	480951.5	4199125H1	308	611
25	480951.5	466549H1	331	540
25	480951.5	3571943H1	331	479
25	480951.5	2943245H2	2145	2471

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
25	480951.5	536022H1	2145	2426
25	480951.5	2961678H1	2154	2478
25	480951.5	2099720H1	2160	2467
25	480951.5	5875882H1	2164	2467
25	480951.5	2531822H1	2174	2510
25	480951.5	772953F1	2178	2736
25	480951.5	g2820897	2184	2741
25	480951.5	1710502H1	2185	2468
25	480951.5	1291521H1	2190	2464
25	480951.5	g794676	2193	2517
25	480951.5	1916675H1	2191	2510
25	480951.5	g787672	2193	2560
25	480951.5	g2204645	2197	2461
25	480951.5	g2839081	2205	2711
25	480951.5	2126621H1	2208	2531
25	480951.5	g2156454	2210	2741
25	480951.5	g2458421	2212	2739
25	480951.5	1834518H1	2217	2484
25	480951.5	3816120H1	2219	2514
25	480951.5	g2992797	2220	2736
25	480951.5	2158693H1	2224	2494
25	480951.5	g1328891	2235	2746
25	480951.5	g2221416	2227	2516
25	480951.5	g1313752	2237	2746
25	480951.5	g3648207	2237	2740
25	480951.5	708349H1	2241	2571
25	480951.5	5057841H1	2241	2545
25	480951.5	g1313306	2257	2743
25	480951.5	g1328885	2297	2746
25	480951.5	g1319439	2304	2736
25	480951.5	g2750733	2309	2725
25	480951.5	g4308069	2319	2742
25	480951.5	g2883660	2320	2743
25	480951.5	4698908H1	2320	2616
25	480951.5	g3037326	2326	2738
25	480951.5	g2162162	2337	2740
25	480951.5	3671211H1	2336	2687
25	480951.5	g2051249	2337	2741
25	480951.5	3092677H1	2336	2643
25	480951.5	g2841059	2337	2742
25	480951.5	5660220H1	2337	2544
25	480951.5	498999H1	2337	2551
25	480951.5	1633006H1	2337	2556
25	480951.5	3026659H1	2336	2662
25	480951.5	564552H1	2337	2576
25	480951.5	g2177724	2337	2737
25	480951.5	g2907272	2337	2738
25	480951.5	g3427370	2337	2736
25	480951.5	g3701416	2337	2735
25	480951.5	g2713691	2337	2736

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
25	480951.5	g3677845	2337	2735
25	480951.5	g4137050	2337	2736
25	480951.5	g4190652	2337	2736
25	480951.5	g2410477	2337	2736
25	480951.5	g2159482	2337	2725
25	480951.5	2024457H1	2337	2573
25	480951.5	497715H1	2338	2641
25	480951.5	4972011H1	2337	2572
25	480951.5	3889752H1	2337	2600
25	480951.5	g4307373	2337	2737
25	480951.5	g923082	2341	2732
25	480951.5	g1319066	2350	2742
25	480951.5	1369972H1	2367	2620
25	480951.5	168757H1	1502	1860
25	480951.5	146107H1	1517	1705
25	480951.5	4175742H1	1513	1829
25	480951.5	516463H1	1522	1773
25	480951.5	1837209H1	1541	1754
25	480951.5	5104267H1	1548	1851
25	480951.5	g1493944	1549	1682
25	480951.5	4828067H1	1560	1843
25	480951.5	3626933H1	1560	1675
25	480951.5	4827669H1	1560	1763
25	480951.5	802254H1	1571	1839
25	480951.5	5733222H1	1573	1667
25	480951.5	1833804H1	1572	1840
25	480951.5	1834116H1	1599	1830
25	480951.5	1834116R6	1599	2021
25	480951.5	2267528H1	1600	1776
25	480951.5	g2047293	1601	2121
25	480951.5	4316354H1	1601	1957
25	480951.5	2531080H1	1614	1859
25	480951.5	3549819H1	1626	1873
25	480951.5	4405261H1	1664	1936
25	480951.5	2595202T6	1667	2181
25	480951.5	2443532H1	1670	1916
25	480951.5	g2205045	1689	2201
25	480951.5	4652128H1	1711	1862
25	480951.5	g2178101	1716	2097
25	480951.5	4540165H1	1743	2004
25	480951.5	019674H1	1751	1969
25	480951.5	5777532H1	1751	2031
25	480951.5	4247819H1	1751	2025
25	480951.5	4244210H1	1751	2022
25	480951.5	139108H1	1751	2091
25	480951.5	1365087R1	1765	2020
25	480951.5	4872832H1	1766	2045
25	480951.5	4182858H1	1766	2029
25	480951.5	1365087H1	1766	2008
25	480951.5	2500845H1	1774	2016

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
25	480951.5	3270008H1	1787	2060
25	480951.5	3026939H1	1801	1902
25	480951.5	1970095F6	1808	2308
25	480951.5	1970095H1	1808	2104
25	480951.5	451299H1	1823	2050
25	480951.5	g1367292	1825	2249
25	480951.5	3400713H1	1828	1918
25	480951.5	5035969H1	1856	2063
25	480951.5	g2986154	1859	2230
25	480951.5	772953R1	1859	2460
25	480951.5	772953H1	1859	2099
25	480951.5	3478925H1	1862	2201
25	480951.5	499186H1	1864	1957
25	480951.5	497679H1	1871	2087
25	480951.5	499991H1	1871	2088
25	480951.5	5119583H1	1894	2180
25	480951.5	g3739696	1903	2235
25	480951.5	5013206H1	1910	2182
25	480951.5	2506884H1	1911	2150
25	480951.5	4728147H1	1911	2162
25	480951.5	2506516H1	1911	2154
25	480951.5	g922543	1923	2226
25	480951.5	g885013	1923	2312
25	480951.5	1220669H1	1928	2075
25	480951.5	3376313H1	1933	2196
25	480951.5	4816025H1	1934	2190
25	480951.5	g2208341	1941	2229
25	480951.5	633621H1	1947	2203
25	480951.5	g2005941	1953	2215
25	480951.5	3882972H1	1967	2274
25	480951.5	g3678005	1967	2227
25	480951.5	4881031H1	1967	2245
25	480951.5	g1102777	1976	2199
25	480951.5	2695882H1	1983	2290
25	480951.5	g2016849	1983	2261
25	480951.5	4607680H1	1986	2257
25	480951.5	3480738H1	1991	2125
25	480951.5	g1506305	2019	2162
25	480951.5	633694H1	2022	2300
25	480951.5	4210591H1	2027	2317
25	480951.5	4758948H1	2028	2334
25	480951.5	563634H1	2039	2256
25	480951.5	1541096H1	2049	2203
25	480951.5	4060004H1	2052	2340
25	480951.5	1970095T6	2057	2694
25	480951.5	1834116T6	2057	2689
25	480951.5	2594078H1	2062	2308
25	480951.5	2452635H1	2067	2319
25	480951.5	2134382H1	2082	2275
25	480951.5	4858857H1	2084	2408

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
25	480951.5	4767365H1	2083	2401
25	480951.5	2289353H1	2085	2322
25	480951.5	1818948H1	2085	2401
25	480951.5	1818322H1	2085	2308
25	480951.5	2972228H2	2086	2308
25	480951.5	2969484H1	2087	2415
25	480951.5	1720287H1	2095	2322
25	480951.5	g1690725	2095	2526
25	480951.5	3702645H1	2105	2416
25	480951.5	625400H1	2105	2308
25	480951.5	3093179H1	2105	2407
25	480951.5	5375221H1	2142	2426
25	480951.5	3228787H1	2143	2261
25	480951.5	g3959433	1122	1538
25	480951.5	5004750H1	1127	1317
25	480951.5	2508409H1	1131	1244
25	480951.5	2073090H1	1131	1460
25	480951.5	2875436H1	1130	1406
25	480951.5	5574295H1	1134	1401
25	480951.5	069957H1	1135	1359
25	480951.5	g1720206	1141	1667
25	480951.5	g2903027	1144	1664
25	480951.5	2964463H1	1147	1500
25	480951.5	g1425708	1165	1667
25	480951.5	g4152996	1175	1667
25	480951.5	g3693187	1178	1667
25	480951.5	g4152993	1178	1667
25	480951.5	679425H1	1181	1468
25	480951.5	630229H1	1186	1458
25	480951.5	g2659963	1190	1609
25	480951.5	g3678646	1190	1680
25	480951.5	4060761H1	1193	1488
25	480951.5	g2161517	1193	1664
25	480951.5	2126237H1	1193	1470
25	480951.5	g3366968	1197	1667
25	480951.5	g4079071	1198	1676
25	480951.5	g3675935	1199	1673
25	480951.5	g3174345	1199	1672
25	480951.5	378369H1	1200	1467
25	480951.5	451941H1	1203	1427
25	480951.5	g1126660	1203	1666
25	480951.5	g2409946	1201	1665
25	480951.5	g2836409	1204	1676
25	480951.5	4380896H1	1205	1426
25	480951.5	g2167291	1205	1676
25	480951.5	g990603	1208	1624
25	480951.5	g1721518	1208	1682
25	480951.5	g2785589	1209	1667
25	480951.5	g3884848	1214	1675
25	480951.5	g2161366	1216	1667

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
25	480951.5	g2714918	1220	1607
25	480951.5	510978H1	1224	1467
25	480951.5	g2741372	1226	1682
25	480951.5	1648008H1	1229	1467
25	480951.5	1648031H1	1229	1456
25	480951.5	2860452H1	1229	1532
25	480951.5	2044321H1	1230	1493
25	480951.5	4216861H1	1230	1528
25	480951.5	880261R1	1246	1854
25	480951.5	880261H1	1246	1589
25	480951.5	497500H1	1247	1588
25	480951.5	562595H1	1247	1491
25	480951.5	390816H1	1247	1513
25	480951.5	3336103H1	1248	1539
25	480951.5	855828R1	655	1282
25	480951.5	855828H1	655	901
25	480951.5	1660116H1	662	903
25	480951.5	4459507H1	664	939
25	480951.5	g892912	664	1073
25	480951.5	1660036H1	662	807
25	480951.5	2737280H1	667	927
25	480951.5	2243455H1	666	953
25	480951.5	3051410H1	678	1002
25	480951.5	g892899	685	983
25	480951.5	1255907H1	715	969
25	480951.5	2687937H1	720	980
25	480951.5	2271346H1	722	999
25	480951.5	3373291H1	332	592
25	480951.5	5292779H2	332	602
25	480951.5	g2013066	334	618
25	480951.5	2235148F6	335	829
25	480951.5	2235148H1	335	596
25	480951.5	g2035111	335	522
25	480951.5	4891424H1	336	638
25	480951.5	5593759H1	338	591
25	480951.5	3390870H1	340	659
25	480951.5	1360005F1	342	875
25	480951.5	2913426H1	342	624
25	480951.5	4770833H1	341	626
25	480951.5	3250802H1	341	670
25	480951.5	1360005H1	342	601
25	480951.5	4023870H1	342	625
25	480951.5	g1998895	343	510
25	480951.5	4161775H1	343	605
25	480951.5	4031302H1	342	614
25	480951.5	3778265H1	342	677
25	480951.5	4843784H1	345	640
25	480951.5	3533957H1	347	688
25	480951.5	451527H1	349	499
25	480951.5	4618672H1	349	614

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
25	480951.5	g2669182	350	825
25	480951.5	g1277584	354	894
25	480951.5	3321371H1	354	659
25	480951.5	2581094H1	355	608
25	480951.5	4729423H1	355	520
25	480951.5	g1799076	359	866
25	480951.5	2457980H1	359	613
25	480951.5	5538138H1	361	523
25	480951.5	3123678H1	357	683
25	480951.5	3123878H1	357	553
25	480951.5	3591022H1	361	693
25	480951.5	3987391H1	362	656
25	480951.5	5391147H1	362	688
25	480951.5	3593512H1	362	715
25	480951.5	407591H1	363	527
25	480951.5	2650347H1	362	618
25	480951.5	1320037H1	362	652
25	480951.5	595420H1	362	628
25	480951.5	2719839H1	362	637
25	480951.5	2885143H1	364	649
25	480951.5	3538760H1	363	592
25	480951.5	4205158H1	362	667
25	480951.5	5064082H1	364	594
25	480951.5	4160969H1	364	672
25	480951.5	3394195H1	364	654
25	480951.5	5542680H1	363	598
25	480951.5	4067217H1	365	659
25	480951.5	1989538H1	367	723
25	480951.5	5395039H1	366	657
25	480951.5	3385558H1	367	659
25	480951.5	3574186H1	367	665
25	480951.5	3765155H1	367	711
25	480951.5	5538463H2	366	572
25	480951.5	1371886H1	367	607
25	480951.5	3291484H1	785	1029
25	480951.5	3984729H1	795	982
25	480951.5	g1303165	796	1092
25	480951.5	3678810H1	803	1029
25	480951.5	3441626H1	804	1029
25	480951.5	3674810H1	805	1005
25	480951.5	1909062H1	806	1029
25	480951.5	g782156	819	1142
25	480951.5	3322168H1	834	1141
25	480951.5	5661420H1	775	1049
25	480951.5	3825020H1	783	1029
25	480951.5	5538458H2	837	997
25	480951.5	754038H1	839	1029
25	480951.5	5516018H1	839	1029
25	480951.5	1727177H1	839	1029
25	480951.5	754038R1	839	1469

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
25	480951.5	999590H1	845	1029
25	480951.5	2780282H1	855	1029
25	480951.5	g2167709	862	1417
25	480951.5	2100719H1	876	1136
25	480951.5	3532184H1	890	1182
25	480951.5	2935763H1	890	1196
25	480951.5	g1844616	891	1232
25	480951.5	g1720287	892	1280
25	480951.5	5212745H1	895	1086
25	480951.5	g897017	902	1334
25	480951.5	341998H1	907	1167
25	480951.5	g2025152	911	1204
25	480951.5	083270H1	918	1140
25	480951.5	2435281H1	955	1204
25	480951.5	g1328982	969	1408
25	480951.5	3837044H1	970	1255
25	480951.5	1600531H1	973	1209
25	480951.5	223514816	1062	1629
25	480951.5	842348R1	1062	1639
25	480951.5	2042383H1	1067	1375
25	480951.5	2376168H1	1069	1226
25	480951.5	2043947H1	1067	1363
25	480951.5	3217005H1	1069	1341
25	480951.5	2374982H1	1069	1266
25	480951.5	2376160H1	1069	1231
25	480951.5	5471168H1	1069	1273
25	480951.5	054106H1	1069	1255
25	480951.5	1719624H1	1069	1229
25	480951.5	842348H1	1069	1294
25	480951.5	2374615H1	1069	1261
25	480951.5	3170061H1	1069	1319
25	480951.5	5158959T6	1071	1642
25	480951.5	1330830H1	1090	1355
25	480951.5	2350109H1	1103	1315
25	480951.5	453412H1	1109	1211
25	480951.5	3421220H1	1115	1377
25	480951.5	507765H1	1118	1339
25	480951.5	198875716	1117	1617
25	480951.5	g1163670	451	632
25	480951.5	2779615H1	479	774
25	480951.5	3211910H1	481	620
25	480951.5	2232343H1	498	762
25	480951.5	g1494000	498	688
25	480951.5	g1670312	497	784
25	480951.5	2705619H1	498	797
25	480951.5	g1278591	498	665
25	480951.5	g1721860	498	940
25	480951.5	g989068	508	801
25	480951.5	g1809515	527	1029
25	480951.5	2944225H1	537	875

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
25	480951.5	2544567H2	534	828
25	480951.5	2499468H1	541	840
25	480951.5	1592175H1	544	772
25	480951.5	1591703H1	544	770
25	480951.5	4176769H1	545	750
25	480951.5	g1156402	547	807
25	480951.5	3322962H1	554	866
25	480951.5	3331328H1	562	726
25	480951.5	3470714H1	560	853
25	480951.5	3214025H1	569	847
25	480951.5	037805H1	572	775
25	480951.5	5401247H1	576	884
25	480951.5	5410853H1	575	857
25	480951.5	5695792H1	620	892
25	480951.5	5294959H1	621	891
25	480951.5	g4310946	625	1135
25	480951.5	g3178543	627	1019
25	480951.5	452965H1	628	866
25	480951.5	3111016H1	632	748
25	480951.5	5208639H1	632	924
25	480951.5	g4194092	641	990
25	480951.5	986785R1	644	1138
25	480951.5	986785H1	644	883
25	480951.5	g1687504	654	1111
25	480951.5	g1064548	657	1032
25	480951.5	3504819H1	369	704
25	480951.5	3800372H1	367	682
25	480951.5	2448255H1	367	621
25	480951.5	2599377H1	366	661
25	480951.5	2741956H1	367	640
25	480951.5	4374001H1	367	688
25	480951.5	2520140H1	369	622
25	480951.5	3751944H1	368	588
25	480951.5	4786273H2	368	561
25	480951.5	2878674H1	370	668
25	480951.5	3119978H1	370	667
25	480951.5	2047646H1	370	648
25	480951.5	4170133H1	370	679
25	480951.5	g981973	372	660
25	480951.5	2898280H1	371	596
25	480951.5	3363180H1	370	650
25	480951.5	g2025536	372	690
25	480951.5	g1198636	372	734
25	480951.5	3649034H1	370	547
25	480951.5	3551711H1	372	703
25	480951.5	1346252H1	374	615
25	480951.5	2441829H1	375	601
25	480951.5	g1974420	378	766
25	480951.5	g1718741	379	696
25	480951.5	3745122H1	378	714

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
25	480951.5	491592H1	380	540
25	480951.5	2921720H1	380	669
25	480951.5	650429H1	380	639
25	480951.5	5224648H1	381	485
25	480951.5	3331491H1	382	646
25	480951.5	4770049H1	388	686
25	480951.5	g2166364	390	811
25	480951.5	5589241H1	390	636
25	480951.5	5542605H1	392	629
25	480951.5	2742261H1	394	688
25	480951.5	5395040H1	393	688
25	480951.5	1579085H1	394	592
25	480951.5	g1147442	397	762
25	480951.5	3726996H1	404	727
25	480951.5	g1146694	404	792
25	480951.5	3647806H1	403	758
25	480951.5	2133705H1	402	688
25	480951.5	1423332H1	404	669
25	480951.5	2020306F6	404	842
25	480951.5	g1978134	404	754
25	480951.5	g1625996	404	807
25	480951.5	2020306H1	404	716
25	480951.5	g1068989	408	782
25	480951.5	3541674H1	409	753
25	480951.5	2664883H1	407	682
25	480951.5	2535301H1	407	675
25	480951.5	g1313751	408	760
25	480951.5	g1367340	409	852
25	480951.5	g1972153	411	675
25	480951.5	3247844H1	410	739
25	480951.5	5545462H1	410	629
25	480951.5	g1425731	411	952
25	480951.5	3140608H1	410	727
25	480951.5	4415741H1	412	699
25	480951.5	5545632H1	413	665
25	480951.5	5041074H1	434	715
25	480951.5	1236401F6	444	920
25	480951.5	1236075F1	444	1124
25	480951.5	1236075H1	444	724
25	480951.5	4747674H1	402	706
25	480951.5	3565518H1	401	740
25	480951.5	4174839H1	402	717
25	480951.5	4418643H1	402	695
25	480951.5	2729711H1	403	690
25	480951.5	3326928H1	403	703
25	480951.5	4822653H1	402	697
25	480951.5	1988757R6	404	842
25	480951.5	3758338H1	403	732
25	480951.5	1988757H1	404	722
25	480951.5	4842127H1	403	693

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
26	481257.3	5091990H1	1	268
26	481257.3	4179591F6	1	484
26	481257.3	3561677F6	103	511
26	481257.3	3561677H1	105	308
26	481257.3	g1624544	108	400
26	481257.3	4765172H1	138	377
26	481257.3	4766669H1	138	352
26	481257.3	4619167H1	243	524
26	481257.3	2537458H1	295	568
26	481257.3	3228346H1	330	603
26	481257.3	g1985467	349	684
26	481257.3	2169847F6	499	895
26	481257.3	2169847H1	499	719
26	481257.3	2527973H1	527	884
26	481257.3	4712652H1	554	800
26	481257.3	g1997026	580	924
26	481257.3	g1996603	580	736
26	481257.3	g707845	629	877
26	481257.3	3438719H1	648	902
26	481257.3	3393125H1	675	922
26	481257.3	2443235H1	693	879
26	481257.3	g2206683	692	1113
26	481257.3	g2183347	692	952
26	481257.3	g2142295	707	1150
26	481257.3	3039414H1	723	989
26	481257.3	2049674H1	748	1005
26	481257.3	3354726H1	748	1038
26	481257.3	5501685H1	785	1050
26	481257.3	5501786H1	785	996
26	481257.3	489168H1	788	1038
26	481257.3	4802557H1	861	1118
26	481257.3	2550396H1	873	1120
26	481257.3	g838984	907	1182
26	481257.3	3393352H1	914	1132
26	481257.3	2645117F6	936	1190
26	481257.3	2645117H1	936	1189
26	481257.3	5507207H1	937	989
26	481257.3	g1960242	952	1533
26	481257.3	1839873H1	1083	1324
26	481257.3	3386853H1	1099	1393
26	481257.3	5538387H1	1101	1297
26	481257.3	5539981H2	1119	1255
26	481257.3	526475H1	1160	1441
26	481257.3	g707846	1162	1504
26	481257.3	4230254H1	1171	1358
26	481257.3	1944021H1	1184	1441
26	481257.3	065494H1	1196	1375
26	481257.3	2443315H1	1209	1452
26	481257.3	4956366H1	1217	1434
26	481257.3	1626283H1	1219	1424

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
26	481257.3	4803693H1	1231	1418
26	481257.3	4803661H1	1231	1463
26	481257.3	2490053H1	1284	1533
26	481257.3	774900R1	1290	1870
26	481257.3	774900H1	1290	1521
26	481257.3	5544123H1	1332	1470
26	481257.3	5543325H2	1332	1537
26	481257.3	882706H1	1373	1639
26	481257.3	2135058H1	1376	1660
26	481257.3	2135057H1	1376	1660
26	481257.3	4756042H1	1378	1638
26	481257.3	3224551H2	1385	1665
26	481257.3	1837721H1	1476	1754
26	481257.3	4700765H1	1496	1767
26	481257.3	5278213H1	1625	1796
26	481257.3	4605663H1	1509	1771
26	481257.3	1258053H1	1644	1882
26	481257.3	g1332248	1519	1971
26	481257.3	3482768H1	1667	1986
26	481257.3	3117425H1	1674	1973
26	481257.3	g2162252	1679	2116
26	481257.3	g773044	1708	1881
26	481257.3	g773045	1709	2008
26	481257.3	g773043	1709	1958
26	481257.3	g776171	1709	2021
26	481257.3	5633438H1	1583	1813
26	481257.3	6063131H1	1710	2045
26	481257.3	4322029H1	1712	1984
26	481257.3	1293678H1	1731	2003
26	481257.3	5633470H1	1584	1851
26	481257.3	g2138927	1742	2131
26	481257.3	5697876H1	1745	2017
26	481257.3	5424544H1	1599	1865
26	481257.3	4752662H1	1764	2045
26	481257.3	265691H1	1779	2037
26	481257.3	2570491H1	1777	2038
26	481257.3	g1924668	1788	2046
26	481257.3	g2155625	1796	2117
26	481257.3	681712H1	1800	2072
26	481257.3	5872540H1	1813	2117
26	481257.3	g840128	1828	2129
26	481257.3	5424549H1	1599	1865
26	481257.3	4114541H1	1600	1904
26	481257.3	g838985	1833	2082
26	481257.3	3113085H1	1839	2137
26	481257.3	g1740712	1845	2006
26	481257.3	4434102H1	1851	2116
26	481257.3	2818414H1	1611	1919
26	481257.3	2699486H1	1876	1990
26	481257.3	2705722H1	1877	2161

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
26	481257.3	4164453H1	1881	2158
26	481257.3	3485863H1	1906	2199
26	481257.3	5086162H1	1920	2106
26	481257.3	3011128H1	1625	1923
26	481257.3	1341459H1	1921	2164
26	481257.3	g879545	1936	2238
26	481257.3	5408150H1	1952	2059
26	481257.3	g2206845	1971	2134
26	481257.3	018589H1	1977	2279
26	481257.3	g2004226	1982	2334
26	481257.3	2474254H1	1988	2230
26	481257.3	1438403H1	1997	2261
26	481257.3	1437601H1	1997	2273
26	481257.3	5154866H1	1998	2251
26	481257.3	1738907F6	2021	2405
26	481257.3	g2031584	2022	2286
26	481257.3	1738907H1	2021	2268
26	481257.3	g873349	2043	2114
26	481257.3	2219963H1	2044	2310
26	481257.3	5546018H1	2057	2260
26	481257.3	4515045H1	2062	2322
26	481257.3	3377306H1	2074	2365
26	481257.3	g1860563	2075	2168
26	481257.3	3931048H1	2082	2386
26	481257.3	655184H1	2532	2780
26	481257.3	4759972H1	2535	2830
26	481257.3	3163986H1	2546	2816
26	481257.3	2425109H1	2548	2790
26	481257.3	1724276H1	2552	2776
26	481257.3	g1887641	2557	2981
26	481257.3	g2820788	2558	2990
26	481257.3	5677886H1	2559	2813
26	481257.3	4904046H2	2561	2845
26	481257.3	3563946H1	2562	2858
26	481257.3	1631524H1	2562	2794
26	481257.3	3563302H1	2562	2889
26	481257.3	g1859585	2571	2997
26	481257.3	1846040H1	2574	2816
26	481257.3	2771788H1	2575	2822
26	481257.3	4802918H1	2576	2839
26	481257.3	350681H1	2581	2797
26	481257.3	2325487H1	2590	2841
26	481257.3	g1977173	2593	2869
26	481257.3	g1892411	2593	2864
26	481257.3	3473745H1	2595	2844
26	481257.3	1863330H1	2595	2846
26	481257.3	1863330F6	2595	3145
26	481257.3	552764H1	2619	2851
26	481257.3	2362444H1	2632	2909
26	481257.3	1745503H1	2635	2883

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
26	481257.3	4558555H1	2639	2891
26	481257.3	532059H1	2639	2854
26	481257.3	4555552H1	2639	2860
26	481257.3	4505643H1	2651	2943
26	481257.3	3068819H1	2656	2975
26	481257.3	3171027H1	2657	2944
26	481257.3	3171088H1	2657	2938
26	481257.3	3379612H1	2660	2928
26	481257.3	g4395482	2684	3050
26	481257.3	1729555H1	2685	2905
26	481257.3	292475H1	2687	3033
26	481257.3	291878H1	2687	2952
26	481257.3	3950881H1	2693	2873
26	481257.3	3012122H1	2695	2981
26	481257.3	547518H1	2695	2933
26	481257.3	4211183H1	2695	2956
26	481257.3	1314982H1	2696	2940
26	481257.3	3946155H1	2700	2877
26	481257.3	6064507H1	2727	2975
26	481257.3	2600642H1	2727	3009
26	481257.3	6064407H1	2727	3024
26	481257.3	3886104H1	2738	3000
26	481257.3	g1893892	2738	3076
26	481257.3	040482H1	2739	2939
26	481257.3	g1892555	2742	3039
26	481257.3	1424170H1	2746	2986
26	481257.3	g1398711	2751	2874
26	481257.3	1759965H1	2762	3034
26	481257.3	g1919966	2768	3113
26	481257.3	696972H1	2768	3064
26	481257.3	3202809H1	2768	3059
26	481257.3	696677H1	2768	3005
26	481257.3	2158950H1	2768	3072
26	481257.3	5167705H1	2781	2881
26	481257.3	2022007H1	2789	3057
26	481257.3	3714681H1	2802	3077
26	481257.3	3761940H1	2802	3098
26	481257.3	3919253H1	2802	3050
26	481257.3	1318693H1	2805	2891
26	481257.3	2284086H1	2829	3055
26	481257.3	1420843H1	2835	3087
26	481257.3	4092117H1	2864	3094
26	481257.3	3366654H1	2203	2492
26	481257.3	g2155929	2204	2638
26	481257.3	3076013H1	2210	2508
26	481257.3	3681116H1	2238	2555
26	481257.3	1747569H1	2272	2555
26	481257.3	1459994H1	2279	2530
26	481257.3	4321951H1	2280	2557
26	481257.3	3723672H1	2280	2463

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
26	481257.3	920433H1	2280	2595
26	481257.3	4622265H1	2285	2462
26	481257.3	338447H1	2287	2535
26	481257.3	g715010	2288	2600
26	481257.3	338842H1	2287	2501
26	481257.3	1351650H1	2288	2546
26	481257.3	1809511F6	2301	2879
26	481257.3	1809511H1	2301	2557
26	481257.3	1553819H1	2306	2506
26	481257.3	3686776H1	2309	2607
26	481257.3	3089582H1	2315	2616
26	481257.3	4903640H1	2327	2616
26	481257.3	1807852H1	2334	2472
26	481257.3	1603388H1	2346	2556
26	481257.3	2585721H1	2346	2608
26	481257.3	490934H1	2347	2614
26	481257.3	4861461H1	2347	2602
26	481257.3	3738138H1	2362	2656
26	481257.3	3749039H1	2368	2654
26	481257.3	2411583H1	2383	2619
26	481257.3	1524008H1	2391	2650
26	481257.3	291952H1	2393	2726
26	481257.3	5569863H1	2396	2629
26	481257.3	658020H1	2399	2657
26	481257.3	2893849H1	2398	2615
26	481257.3	1544390H1	2400	2604
26	481257.3	2440744H1	2415	2645
26	481257.3	2185706H1	2427	2711
26	481257.3	g1687360	2442	2876
26	481257.3	4904656H2	2457	2731
26	481257.3	3929576H1	2460	2755
26	481257.3	2743452H1	2479	2746
26	481257.3	2441476H1	2479	2708
26	481257.3	4558022H1	2511	2784
26	481257.3	4073134H1	2512	2712
26	481257.3	2188345H1	2519	2793
26	481257.3	4375649H1	2523	2788
26	481257.3	g1860487	2524	2741
26	481257.3	2618351H1	2531	2774
26	481257.3	4880013H1	3083	3371
26	481257.3	3931126H1	2082	2372
26	481257.3	2156566H1	2092	2377
26	481257.3	3931010H1	2082	2262
26	481257.3	5156451H1	2112	2368
26	481257.3	5779103H1	2082	2363
26	481257.3	667400H1	2093	2357
26	481257.3	g1898178	2093	2458
26	481257.3	663114H1	2123	2398
26	481257.3	663147H1	2123	2406
26	481257.3	4758209H1	2124	2413

TABLE 3

SEQ ID NO:	Template ID	Component ID	Start	Stop
26	481257.3	2797741H1	2128	2388
26	481257.3	5205492H2	2135	2389
26	481257.3	528572H1	2138	2414
26	481257.3	2495479H1	2139	2385
26	481257.3	4513333H1	2154	2422
26	481257.3	3771907H1	2167	2496
26	481257.3	5208347H1	2180	2439
26	481257.3	1390911H1	2187	2445

Table 4

Program	Description	Reference	Parameter Threshold
ABI FACTURA	A program that removes vector sequences and masks ambiguous bases in nucleic acid sequences.	PE Biosystems, Foster City, CA.	
ABI/PARACEL FDF	A Fast Data Finder useful in comparing and annotating amino acid or nucleic acid sequences.	PE Biosystems, Foster City, CA; Paracel Inc., Pasadena, CA.	Mismatch <50%
ABI AutoAssembler	A program that assembles nucleic acid sequences.	PE Biosystems, Foster City, CA.	
BLAST	A Basic Local Alignment Search Tool useful in sequence similarity search for amino acid and nucleic acid sequences. BLAST includes five functions: blastp, blastn, blastx, tblastn, and tblastx.	Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410; Altschul, S.F. et al. (1997) Nucleic Acids Res. 25:3389-3402.	*ESTs:* Probability value= 1.0E-8 or less *Full Length sequences*: Probability value= 1.0E-10 or less
FASTA	A Pearson and Lipman algorithm that searches for similarity between a query sequence and a group of sequences of the same type. FASTA comprises as least five functions: fasta, tfasta, fastx, tfastx, and ssearch.	Pearson, W.R. and D.J. Lipman (1988) Proc. Natl. Acad Sci. USA 85:2444-2448; Pearson, W.R. (1990) Methods Enzymol. 183:63-98; and Smith, T.F. and M.S. Waterman (1981) Adv. Appl. Math. 2:482-489.	*ESTs:* fasta E value=1.06E-6 *Assembled ESTs*: fasta Identity= 95% or greater and Match length=200 bases or greater; fastx E value=1.0E-8 or less *Full Length sequences:* fastx score=100 or greater
BLIMPS	A BLocks IMProved Searcher that matches a sequence against those in BLOCKS, PRINTS, DOMO, PRODOM, and PFAM databases to search for gene families, sequence homology, and structural fingerprint regions.	Henikoff, S. and J.G. Henikoff (1991) Nucleic Acids Res. 19:6565-6572; Henikoff, J.G. and S. Henikoff (1996) Methods Enzymol. 266:88-105; and Attwood, T.K. et al. (1997) J. Chem. Inf. Comput. Sci. 37:417-424.	Score=1000 or greater; Ratio of Score/Strength = 0.75 or larger; and, if applicable, Probability value= 1.0E-3 or less
HMMER	An algorithm for searching a query sequence against hidden Markov model (HMM)-based databases of protein family consensus sequences, such as PFAM.	Krogh, A. et al. (1994) J. Mol. Biol. 235:1501-1531; Sonnhammer, E.L.L. et al. (1988) Nucleic Acids Res. 26:320-322.	Score=10-50 bits for PFAM hits, depending on individual protein families

Table 4 (cont.)

Program	Description	Reference	Parameter Threshold
ProfileScan	An algorithm that searches for structural and sequence motifs in protein sequences that match sequence patterns defined in Prosite.	Gribskov, M. et al. (1988) CABIOS 4:61-66; Gribskov, M. et al. (1989) Methods Enzymol. 183:146-159; Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221.	Normalized quality score≥GCG-specified "HIGH" value for that particular Prosite motif. Generally, score=1.4-2.1.
Phred	A base-calling algorithm that examines automated sequencer traces with high sensitivity and probability.	Ewing, B. et al. (1998) Genome Res. 8:175-185; Ewing, B. and P. Green (1998) Genome Res. 8:186-194.	
Phrap	A Phils Revised Assembly Program including SWAT and CrossMatch, programs based on efficient implementation of the Smith-Waterman algorithm, useful in searching sequence homology and assembling DNA sequences.	Smith, T.F. and M.S. Waterman (1981) Adv. Appl. Math. 2:482-489; Smith, T.F. and M.S. Waterman (1981) J. Mol. Biol. 147:195-197; and Green, P., University of Washington, Seattle, WA.	Score= 120 or greater; Match length= 56 or greater
Consed	A graphical tool for viewing and editing Phrap assemblies.	Gordon, D. et al. (1998) Genome Res. 8:195-202.	
SPScan	A weight matrix analysis program that scans protein sequences for the presence of secretory signal peptides.	Nielson, H. et al. (1997) Protein Engineering 10:1-6; Claverie, J.M. and S. Audic (1997) CABIOS 12:431-439.	Score=3.5 or greater
Motifs	A program that searches amino acid sequences for patterns that matched those defined in Prosite.	Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221; Wisconsin Package Program Manual, version 9, page M51-59, Genetics Computer Group, Madison, WI.	

CLAIMS

What is claimed is:

1. An isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of:

a) a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-26,

b) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-26,

c) a polynucleotide sequence complementary to a),

d) a polynucleotide sequence complementary to b), and

e) an RNA equivalent of a) through d).

2. An isolated polynucleotide of claim 1, comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-26.

3. An isolated polynucleotide comprising at least 60 contiguous nucleotides of a polynucleotide of claim 1.

4. A composition for the detection of expression of secretory polynucleotides comprising at least one of the polynucleotides of claim 1 and a detectable label.

5. A method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 1, the method comprising:

a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and

b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

6. A method for detecting a target polynucleotide in a sample, said target polynucleotide comprising a sequence of a polynucleotide of claim 1, the method comprising:

a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide, and

b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof.

7. A method of claim 5, wherein the probe comprises at least 30 contiguous nucleotides.

8. A method of claim 5, wherein the probe comprises at least 60 contiguous nucleotides.

9. A recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide of claim 1.

10. A cell transformed with a recombinant polynucleotide of claim 9.

11. A transgenic organism comprising a recombinant polynucleotide of claim 9.

12. A method for producing a secretory polypeptide, the method comprising:

a) culturing a cell under conditions suitable for expression of the secretory polypeptide, wherein said cell is transformed with a recombinant polynucleotide of claim 9, and

b) recovering the secretory polypeptide so expressed.

13. A purified secretory polypeptide (SPTM) encoded by at least one of the polynucleotides of claim 2.

14. An isolated antibody which specifically binds to a secretory polypeptide of claim 13.

15. A method of identifying a test compound which specifically binds to the secretory polypeptide of claim 13, the method comprising the steps of:

a) providing a test compound;

b) combining the secretory polypeptide with the test compound for a sufficient time and under suitable conditions for binding; and

c) detecting binding of the secretory polypeptide to the test compound, thereby identifying the test compound which specifically binds the secretory polypeptide.

16. A microarray wherein at least one element of the microarray is a polynucleotide of claim 3.

17. A method for generating a transcript image of a sample which contains polynucleotides, the method comprising the steps of:

a) labeling the polynucleotides of the sample,

b) contacting the elements of the microarray of claim 16 with the labeled polynucleotides of the sample under conditions suitable for the formation of a hybridization complex, and

c) quantifying the expression of the polynucleotides in the sample.

18. A method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a polynucleotide sequence of claim 1, the method comprising:

a) exposing a sample comprising the target polynucleotide to a compound, and

b) detecting altered expression of the target polynucleotide.

19. A method of claim 6 for toxicity testing of a compound, further comprising:

c) comparing the presence, absence or amount of said target polynucleotide in a first biological sample and a second biological sample, wherein said first biological sample has been contacted with said compound, and said second sample is a control, whereby a change in presence, absence or amount of said target polynucleotide in said first sample, as compared with said second sample, is indicative of toxic response to said compound.

SEQUENCE LISTING

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Banville, Steve C.
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Dufour, Gerard E.
Cohen, Howard J.
Rosen, Bruce
Chalup, Michael S.
Hillman, Jennifer L.
Jones, Anissa L.
Yu, Jimmy Y.
Greenawalt, Lila B.
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<213> Homo sapiens

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<222> 551, 1151, 1200, 1257, 1823
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<212> DNA
<213> Homo sapiens

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<223> Incyte ID No: 335484.1

<220>
<221> unsure
<222> 3222
<223> a, t, c, g, or other

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<211> 1451
<212> DNA
<213> Homo sapiens

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<223> Incyte ID No: 337489.2

<220>
<221> unsure
<222> 281, 291, 830, 845
<223> a, t, c, g, or other

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<212> DNA
<213> Homo sapiens

<220>
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<223> Incyte ID No: 359574.5

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<210> 22
<211> 2271
<212> DNA
<213> Homo sapiens

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<223> Incyte ID No: 360645.5

<220>
<221> unsure
<222> 2002
<223> a, t, c, g, or other

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INTERNATIONAL SEARCH REPORT

Inti inal Application No
PCT/US 00/15246

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12N15/00 C12N15/63 C07K14/47 C07K16/00 C12Q1/68
G01N33/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, EMBL, MEDLINE, EMBASE, BIOSIS, CHEM ABS Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE EMEST_HUM6 [Online] ID:AI638611, 29 April 1999 (1999-04-29) NCI-CGAP: "EST, Homo sapiens cDNA clone IMAGE:2242365" XP002148146	1-3
Y	abstract ---	4-19
X	DATABASE EMEST_HUM4 [Online] ID:AI123547, 8 September 1998 (1998-09-08) NCI-CGAP: "EST,Homo sapiens cDNA clone IMAGE:1690146" XP002148147	1-3
Y	abstract --- -/--	4-19

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

° Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
22 September 2000	08. 01. 2001

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Hagenmaier, S

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INTERNATIONAL SEARCH REPORT

Int nal Application No
PCT/US 00/15246

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE EMEST_HUM15 [Online] ID:HS513324, HILLIER ET AL.: "Homo sapiens cDNA clone IMAGE:278129" XP002148148	1-3
Y	abstract	4-19

Y	WO 99 03990 A (FLORENCE KIMBERLY A ;HUMAN GENOME SCIENCES INC (US); FENG PING (US) 28 January 1999 (1999-01-28) the whole document	4-19

Y	WO 98 25959 A (CHIRON CORP) 18 June 1998 (1998-06-18) the whole document	4-19

Y	WO 99 05256 A (HARVARD COLLEGE) 4 February 1999 (1999-02-04) the whole document	4-19

A	WO 95 20681 A (INCYTE PHARMA INC) 3 August 1995 (1995-08-03) the whole document	

P,X	DATABASE GENESEQ [Online] ID:Z15641/ WO9938972, 5 August 1999 (1999-08-05) CHIRON: " Human gene expression product cDNA Seq. ID 3110" XP002148149 abstract	1-19

Form PCT/ISA/210 (continuation of second sheet) (July 1992)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 00/15246

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

claims 1-19 all partially

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-19 (all partially)

Invention 1:

Isolated polynucleotide comprising a polynucleotide sequence with Seq.ID 1, methods, compositions and microarrays using said polynucleotide, as well as a recombinant polynucleotide comprising a promoter sequence operably linked to Seq.ID 1, a cell and a transgenic organism comprising such a recombinant polynucleotide, a purified secretory polypeptide encoded by Seq.ID 1, a method of producing such a polypeptide, an antibody which specifically binds to this secretory polypeptide as well as methods of identifying a test compound using this polypeptide.

2. Claims: 1-19 (all partially)

Inventions 2-26:

Isolated polynucleotide comprising a polynucleotide sequence with Seq.ID 2, methods, compositions and microarrays using said polynucleotide, as well as a recombinant polynucleotide comprising a promoter sequence operably linked to Seq.ID 2, a cell and a transgenic organism comprising such a recombinant polynucleotide, a purified secretory polypeptide encoded by Seq.ID 2, a method of producing such a polypeptide, an antibody which specifically binds to this secretory polypeptide as well as methods of identifying a test compound using this polypeptide.

..idem for Seq.IDs 3-26

INTERNATIONAL SEARCH REPORT

Information on patent family members

Intern...al Application No
PCT/US 00/15246

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